(19) Europäisches Patentamt
European Patent Office
Office européen des brevets

(11) EP 2 223 936 A1

(12) EUROPEAN PATENT APPLICATION

(43) Date of publication:
01.09.2010 Bulletin 2010/35

(51) Int Cl.:
C07K 14/37 *(2006.01)*

(21) Application number: **09153889.2**

(22) Date of filing: **27.02.2009**

(84) Designated Contracting States:
AT BE BG CH CY CZ DE DK EE ES FI FR GB GR HR HU IE IS IT LI LT LU LV MC MK MT NL NO PL PT RO SE SI SK TR
Designated Extension States:
AL BA RS

(71) Applicants:
- **Universität für Bodenkultur Wien**
  1180 Wien (AT)
- **Angewandte Biokatalyse-Kompetenzzentrum GmbH**
  8010 Graz (AT)
- **Gorton, Lo**
  21155 Malmö (SE)

(72) Inventors:
- **Ludwig, Roland, Dr.**
  1220 Vienna (AT)
- **Gorton, Lo**
  21155 Malmö (SE)
- **Haltrich, Dietmar, Dr.**
  1190 Vienna (AT)
- **Harreither, Wolfgang, DI**
  1200 Vienna (AT)

(74) Representative: **Sonn & Partner Patentanwälte**
Riemergasse 14
1010 Wien (AT)

(54) Cellobiose Dehydrogenase

(57) The present invention relates to cellobiose dehydrogenases (CDH) having glucose oxidation activity at a pH of 7.4 or above, modifications to modify the pH dependency of the enzymes activity, uses for these CDHs, in particular electrode sensors and electrochemical cells.

EP 2 223 936 A1

Description

[0001] The present invention relates to cellobiose dehydrogenase (CDH) enzymes, modifications thereof and electrochemical uses.

[0002] Cellobiose dehydrogenase (EC 1.1.99.18, CDH) was first discovered 1974 in the extracellular enzyme system of *Phanerochaete chrysosporium* and later on in several other basidiomycete fungi. A special characteristic of this enzyme is its composition: the combination of a catalytically active flavin domain, hosting a non-covalently bound FAD, and a haem domain, with a haem b as a cofactor. Both domains are connected by a flexible linker. By its catalytic activity, the substrate, e.g. cellobiose, is oxidised in a reaction which reduces the FAD of the flavin domain. Subsequently, FAD can be reoxidised by the action of the haem domain. The spectral characteristics of a typical CDH clearly show the presence of both cofactors. Another characteristic described is the strong glucose discrimination of all well characterised enzymes. Until the discovery of the ascomycete fungus *Myriococcum thermophilum* (Stoica et al., 2005, Biosensors and Bioelectronics 20: 2010-2018; Harreither et al., 2007, Electroanalysis 19: 172-180), CDH was believed to strongly inhibit the conversion of glucose (Henriksson et al., 1998, Biochimica Biophysica Acta 1383: 48-54). Similarly, for a long time only CDHs exhibiting an acidic activity optimum were known, especially when the haem domain is involved in catalysis as it depends on intramolecular electron transfer (IET), which is necessary to transfer electrons via the haem to the electron acceptor. This is the case with cytochrome c in enzymatic assays, as well as on electrode surfaces where the haem domain enables direct electron transfer (DET) to the electrode.

[0003] Electrochemical applications described in the literature are the detection of cellobiose, cello-oligosaccharides, lactose and maltose soluble cellodextrins, ortho- and para-diphenolic compounds (Lindgren et al., 1999, Analyst 124: 527-532) and catecholamines (Stoica et al., 2004, Analytical Chemistry, 76: 4690-4696) mostly by mediated electron transfer (MET). So far the application in glucose biosensors based on the direct electron transfer (DET) properties of CDH was prevented by i) a very low or no glucose turnover, ii) the acidic pH optimum of most known CDHs and iii) a bad performance of some CDHs on electrodes.

[0004] Although, one CDH with well functioning IET at neutral or alkaline pH values is known (from the fungus *Humicola insolens*), it was shown not to convert glucose (Schou et al., 1998, Biochemical Journal 330: 565-571). One CDH currently known to convert glucose with significant turnover numbers was found in cultures of *Myriococcum thermophilum* (Harreither et al., 2007, Electroanalysis 19: 172-180). However, this enzyme has an acidic pH optimum for the IET and shows no activity under physiological pH conditions (pH 7.4). Another obstruction is the sometimes bad electronic communication of a CDH with an electrode surface, like the *Humicola insolens* and *Sclerotium rolfsii* CDHs (Lindgren et al., 2001, Journal of Electroanalytical Chemistry 496: 76-81), which results in very low current densities and therefore low signals even with high concentrations of the natural substrate cellobiose.

[0005] Thus CDH activity on glucose under neutral conditions, which is necessary for applications in e.g. physiological fluids is not satisfying, in particular not for the electrochemical measurement of glucose or the generation of electricity in biofuel cells. It is therefore a goal of the present invention to provide an alternative enzyme suitable to convert glucose at physiological pH ranges.

[0006] Therefore, in a first embodiment the present invention provides a CDH having glucose oxidation activity at a pH of 7.4 or above, selected from a CDH isolated from *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa* or *Stachybotris bisbyi* or being a modified CDH of *Myriococcum thermophilum.* According to the invention it has been surprisingly found that certain CDHs have a suitable activity under physiological pH conditions. Furthermore, the invention provides the modification of acidic CDHs to increase their activity at pH 7.4 and above.

[0007] The term "cellobiose dehydrogenase" is defined herein as an enzyme consisting of a flavin domain and a haem domain connected by a peptide linker, which oxidises carbohydrates like its natural substrates cellobiose and cello-oligosaccharides and others like lactose, maltose and in particular glucose for preferred inventive uses. The reoxidation of the flavin domain cofactor can be achieved by direct oxidation by two-electron acceptors including quinones like 2,6-dichloroindophenol, *o*- or p-benzoquinone or derivatives thereof, methylene blue, methylene green, Meldola's blue or one-electron acceptors like potassium ferricyanide, ferricenium hexafluorophosphate, $FeCl_3$ or by intramolecular electron transfer (IET) to the haem domain cofactor and further to a terminal electron acceptor like cytochrome *c* (cyt *c*) or an electrode surface.

[0008] The flavin domain of the CDH, which is responsible for the glucose oxidation activity and the haem domain, responsible for the regeneration of the flavin domain, may have two different pH optima, such as in the case of the natural CDH of *Myriococcum thermophilum.* In principle, the haem domain can be bypassed by providing the flavin domain with oxidants such as 2,6-dichloroindophenol which can directly reoxidise the flavin domain without the haem domain. According to the present invention, however, it should be understand that the CDH has a glucose oxidation activity at a pH of 7.4 by the action of both the flavin and the haem domain as can e.g. be measured by the cyt c assay or by measurement after immobilisation on an electrode surface. The haem domain acts as intermediate electron transmitter between cyt c and the flavin domain or between the electrode surface and the flavin domain, respectively.

[0009] The natural, wild-type CDH of *M. thermophilum* does not have the inventive glucose oxidation activity at a pH of 7.4 by action of both the flavin and the haem domain. The present invention has now for the first time provided a modification of the CDH of *M. thermophilum* which has the desired glucose oxidation activity. This modification according to the present invention should now be understood in that the inventive *M. thermophilum* CDH deviates from the wild-type *M. thermophilum* CDH by the substantially increased glucose oxidation activity at a pH of 7.4. This modification can be facilitated by increasing the interaction between the flavin and the haem domains, e.g. by modifying specific key amino acids responsible for that interaction as is further described herein. Preferably increasing the interaction includes increasing contacts or interaction energy between the domains. A prediction of such modifications can be easily made *in silico* using e.g. force field based interaction energy calculations. Furthermore interaction can be determined by measuring protein activity as described herein. Furthermore, it is possible to increase the pH dependency of the haem domain to a more basic pH. The pH optimum of the flavin domain of the natural CDH of *M. thermophilum* could in principle have the required pH properties to oxidise glucose, as is e.g. shown in **Fig. 2f** (by measurement of the 2,6-dichloroindophenol (DCIP)assay).

[0010] Also provided are enzyme preparations comprising novel CDHs. The term "enzyme" or "enzyme preparation" as used herein refers to a cellobiose dehydrogenase from a specified organism which is at least about 20% pure, preferably at least about 40% pure, even more preferably at least about 60% pure, even more preferably at least 80% pure and most preferably at least 90% pure as determined by polyacrylamide gel electrophoresis (PAGE).

[0011] The present invention relates to cellobiose dehydrogenases isolated from novel producers or genetically engineered from existing protein scaffolds, which are able to oxidise glucose more efficiently than the currently known cellobiose dehydrogenases. The kinetic constants of the enzymes responsible for this effect are a preferably lower K_M value and a higher k_{cat} value for glucose than the currently characterised enzymes (e.g., *Phanerochaete chrysosporium* CDH: K_M = 1600 mM, k_{cat} = 2.64 s^{-1}, Henriksson et al., 1998, Biochimica and Biophysica Acta 1383: 48-54; Humicola insolens CDH: no glucose conversion detected, Schou et al., 1998, Biochemical Journal 330: 565-571; *Trametes villosa* CDH: K_M = 1300 mM, k_{cat} = 1.92 s^{-1}, Ludwig et al., 2004, Applied Microbiology and Biotechnology 64: 213-222). In addition, the k_m and k_{cat} values for glucose oxidation of the inventive enzymes shall be at a pH of 7.4.

[0012] In a further aspect the present invention provides a cellobiose dehydrogenase of SEQ ID NO: 5 (*Chaetomium atrobrunneum*), SEQ ID NO: 7 (*Corynascus thermophilum*), SEQ ID NO: 3 (*Hypoxylon haematostroma*), SEQ ID NO: 11 (*Neurospora crassa*) and SEQ ID NO: *9* (*Stachybotrys bisbyi*). Furthermore homologuous enzymes are provided having glucose oxidation activity at a pH of 7.4 or above comprising an amino acid sequence being at least 50%, preferably at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identical to any one of SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11.

[0013] In preferred embodiments the CDH of *Chaetomium atrobrunneum* comprises an amino acid sequence of SEQ ID NO: 5. The CDH is readily available from *C. atrobrunneum* using the isolation methods described herein. In a further related aspect the present invention also provides a CDH comprising an amino acid sequence of SEQ ID NO: 5, or an amino acid sequence being at least 83%, preferably at least 85%, at least 88%, at least 90%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, in particular preferred at least 99%, identical to SEQ ID NO: 5.

[0014] In preferred embodiments the CDH of *Corynascus thermophilum* comprises an amino acid sequence of SEQ ID NO: 7. The CDH is readily available from *C. thermophilum* using the isolation methods described herein. In a further related aspect the present invention also provides a CDH comprising an amino acid sequence of SEQ ID NO: 7, or an amino acid sequence being at least 76%, preferably at least 78%, at least 80%, at least 83%, at least 85%, at least 88%, at least 90%, at least 92%, at least 94%, at least 95%, at least 98%, in particular preferred at least 99%, identical to SEQ ID NO: 7.

[0015] In preferred embodiments the CDH of *Hypoxylon haematostroma* comprises an amino acid sequence of SEQ ID NO: 3. The CDH is readily available from *H. haematostroma* using the isolation methods described herein. In a further related aspect the present invention also provides a CDH comprising an amino acid sequence of SEQ ID NO: 3, or an amino acid sequence being at least 68%, preferably at least 70%, at least 72%, at least 74%, at least 76%, at least 78%, at least 80%, at least 80%, at least 83%, at least 85%, at least 88%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identical to SEQ ID NO: 3.

[0016] In preferred embodiments the CDH of *Neurospora crassa* comprises an amino acid sequence of SEQ ID NO: 11. The CDH is readily available from *N. crassa* using the isolation methods described herein. In a further related aspect the present invention also provides a CDH comprising an amino acid sequence of SEQ ID NO: 11, or an amino acid sequence being at least 72%, preferably at least 74%, at least 76%, at least 78%, at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 92%, at least 95%, at least 98%, in particular preferred at least 99%, identical to SEQ ID NO: 11.

[0017] In preferred embodiments the CDH of *Stachybotrys bisbyi* comprises an amino acid sequence of SEQ ID NO: 9. The CDH is readily available from *S. bisbyi* using the isolation methods described herein. In a further related aspect

the present invention also provides a CDH comprising an amino acid sequence of SEQ ID NO: 9, or an amino acid sequence being at least 59%, preferably at least 60%, at least 62%, at least 65%, at least 70%, at least 72%, preferably at least 74%, at least 76%, at least 78%, at least 80%, at least 82%, at least 84%, at least 86%, at least 88%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identical to SEQ ID NO: 9.

[0018] Preferably, a homologous or modified CDH of has 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, at least 11, at last 13, at least 15, at least 17, at least 20, at least 25, at least 30, at least 40, at least 50, at least 60, at least 80, at least 100 and/or up to 100, up to 80, up to 60, up to 50, up to 40, up to 30, up to 30, up to 20, up to 15 amino acid substitutions, deletions, insertions or modifications, and any ranges between these values, as compared to any one of the CDHs of SEQ ID NOs 3, 5, 7, 9 or 11.

[0019] The present invention provides novel sequences of CDHs from *Chaetomium atrobrunneum* (SEQ ID NO: 5), *Corynascus thermophilum* (SEQ ID NO: 7), *Hypoxylon haematostroma* (SEQ ID NO: 3), *Neurospora crassa* (SEQ ID NO: 11) and *Stachybotrys bisbyi* (SEQ ID NO: 9). The CDHs of these sequences, as well as homologues with at least 50% sequence identity thereto are novel CDHs which also fulfill the inventive properties of having a glucose oxidation activity at a pH of 7.4. The modification of homologuous enzymes thereto with at least 50% sequence identity are preferably of amino acids which do not lower the pH requirement on the glucose oxidation acitivity. Any such modification can easily be tested by a glucose oxidation test on e.g. an electrode surface or by a cyt c assay, using cyt c to reoxidise the haem and subsequently the flavin domain of the CDH. Homologues can be readily identified by sequence comparisons such as by sequence alignment using publicly available tools, such as BLASTP.

[0020] The inventive CDH may be a modified CDH of *Myriococcum thermophilum,* comprising a flavin and a haem domain, wherein electron transfer from the flavin to the haem domain is increased as compared to wild type CDH of *M. thermophilum,* preferably as measured by the cyt c assay. Thus the invention relates to genetic engineering of a CDH to improve the enzymes activity further in the direction of high IET under neutral or alkaline pH conditions. The methods for the modification may be any known in the art such as amino acid mutations, including amino acid substitutions, deletions or additions but also chemical modification/derivatisation of amino acid side chains, in particular acidic amino acid side chains.

[0021] As mentioned above, the invention includes homologuous sequences to the inventive CDHs of SEQ ID NOs 1 (*M. thermophilum* - with further modifications to improve the pH dependency as mentioned above), SEQ ID Nos. 3, 5, 7, 9 or 11 with at least 50%, preferably at least 55%, at least 60%, at lest 65%, at least 70%, at least 75%, at least 80%, at least 85%, preferably at least 90%, at least 95%, at least 98%, or at least 99%, sequence identity to the above sequences of SEQ ID NOs 1, 3, 5, 7, 9, or 11. Preferably the catalytic site has a minimum of modifications of e.g. 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 amino acid deletions, substitutions or additions or is even exempted from modifications as compared to the wild type catalytic sites. The catalytic site is from Phe 251 to Ala 287 (Rossman Fold, flavin binding), Val 334 to Leu 345 and Met 724 to Asp 732 of the *M. thermophilum* sequence of SEQ ID NO: 1. Corresponding amino acids also exist for the CDHs of *Chaetomium atrobrunneum* (SEQ ID NO: *5), Corynascus thermophilum* (SEQ ID NO: 7), *Hypoxylon* haema*tostroma* (SEQ ID NO: 3), *Neurospora crassa* (SEQ ID NO: 11) and *Stachybotrys bisbyi* (SEQ ID NO: 9).

[0022] Preferably any one of the inventive CDHs shows IET (the transfer from electrons from the flavin to the haem domain) under neutral, alkaline or preferentially physiological (pH 7.4) pH conditions. To ensure a sufficiently high electrocatalytic activity of the enzyme under those conditions the IET as measured with the cyt c assay at pH 7.4 should be at least about 10% of the value maximum IET value measured under acidic pH conditions, or more preferably about 20%, or more preferably about 40%, or more preferably about 60%, or even more preferably about 80%, or most preferably should the pH optimum of IET be already neutral or alkaline.

[0023] The cellobiose dehydrogenases show preferably a sufficiently high direct electron transfer (DET) rate from the enzyme to the electrode to obtain a sufficiently high response at low substrate concentrations for a low detection limit and a high sensitivity. Only enzymes exhibiting high enough a DET current at the applied overpotential of +300 mV *v*s. Ag|AgCl (in 0.1 M KC1) to result in a detection limit of glucose (the lower limit of the linear range of the electrode was defined as the detection limit) with a spectrographic graphite electrode setup below 4 mM (the usual blood glucose concentration in a healthy human is 4-7 mM).

[0024] Preferably, the inventive CDH has an glucose oxidation activity at a pH of 7.4 or above and comprises an amino acid sequence of amino acids 22 to 828 of SEQ ID NO: 1 or an amino acid sequence being at least 50%, preferably at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 94%, at least 95%, at least 96%, at least 98%, in particular preferred at least 99%, identical to amino acids 22 to 828 of SEQ ID NO: 1, **characterised in that** the amino acid sequence has at least one additional amino acid substitution, deletion or insertion to the sequence of SEQ ID NO:1 increasing electron transfer from the flavin to the haem domain as compared to wild type CDH of *Myriococcum thermophilum* of SEQ ID NO:1, preferably as measured by the cyt *c* assay. Given in SEQ ID NO: 1 is the wild type *M. thermophilum* CDH which does not have the required glucose oxidation activity at a pH of 7.4. The sequence of SEQ ID NO: 1 has further a signal peptide up to amino acid 21 which may not be present on the final processed enzyme. It could now be shown that according to the present invention by a single (or more)

amino acid substitution, deletion or insertion of the CDH with the final *M. thermophilum* CDH sequence the pH optimum of the glucose oxidation activity can be shifted to a more basic pH, in particular to a physiologically relevant pH of 7.4. Those skilled in the art can readily chose from possible amino acid modifications given the extensive sequence and functional information depicted herein and furthermore, can without undue burden test the modified CDH by a simple cyt c assay as described herein. Preferably, the inventive modified CDH of *M. thermophilum* has 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, at least 11, at last 13, at least 15, at least 17, at least 20, at least 25, at least 30, at least 40, at least 50, at least 60, at least 80, at least 100 and/or up to 100, up to 80, up to 60, up to 50, up to 40, up to 30, up to 30, up to 20, up to 15 amino acid substitutions, deletions, insertions or modifications, and any ranges between these values.

[0025] In a further embodiment the electron transfer of the modified CDH is increased by increasing electrostatic interaction between the flavin and the haem domain, preferably at a pH of 7.4. The electrostatic interaction can be increased by optimising charge interactions at pH 7.4 of basic and acidic amino acids of the flavin and haem domain by site-directed mutagenesis, electrostatic repulsion can be reduced or electrostatic attraction increased. From the available sequence and structural information those skilled in the art can readily chose from a vast amount of such possible mutations which increase the interaction at pH 7.4, and preferably results in an increased activity in a cyt c assay.

[0026] As has been pointed out, the intramolecular electron transfer (IET) rate between the flavin domain and the haem domain depends heavily on the pH. E.g. in the basidiomycete *Trametes villosa* CDH IET is fast at pH 3.5, slows down significantly at pH 5.0, and is virtually absent above pH 6.0. Contrary, the IET of the ascomycete *H. insolens CDH* is not affected by alkaline conditions, having a pH optimum of around 8.0. From the kinetic data of *Humicola insolens CDH* an alkaline pH optimum for cyt c reduction is obvious and the DET measured for that enzyme was highest at pH >7 and is thus an exception so far for CDHs. Interestingly, although an ascomycete CDH, *Myriococcum thermophilum CDH* has an IET behaviour similar to basidiomycete enzymes. Preferably, the above amino acids are modified in the *M. thermophilum* CDH to increase the activity at a pH of 7.4 as measured in a cyt c assay. Furthermore it has been found that these amino acids are of particular interest for the activity of the enzyme. Amino acids corresponding to these amino acids in CDHs of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa* or *Stachybotris bisb*yi with preferably modifications, according to the homologues to the sequences of the SEQ IDs NO: 3, 5, 7, 9 and 11 in other amino acids than in those corresponding to the above amino acids of *Myriococcum thermophilum* of SEQ ID NO: 1.

[0027] The changes in the above mentioned amino acids of SEQ ID NO: 1 in order to increase the activity at pH 7.4 are preferably to increase electrostactic interaction between the flavin and the haem domain as mentioned above.

[0028] In particular preferred embodiments the modification of the CDH is a modification of the haem domain of any one of amino acids 90-100, 115-124, 172-203, preferably of any one of amino acids 176, 179-182, 195, 196, 198, 201 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1 and/or of the flavin domain of any one of amino acids 311-333, 565-577, 623-625, 653-664, 696-723, preferably of any one of amino acids 318, 325, 326, 328, 568, 571, 574, 575, 624, 654, 663, 702, 709, 712, 717, correspond to the *M. thermophilum* CDH of SEQ ID NO: 1, or any combination thereof.

[0029] Possible modifications include (i) the exchange of acidic amino acids by neutral (polar or apolar) residues (e.g. Ser, Thr, Ala) to decrease the number of negative charges and weaken the electrostatic force field at either the haem or the flavin domain at neutral/alkaline pH values. (ii) The exchange of acidic amino acids by alkaline residues (Lys, Arg) to increase the number of positive charges and weaken the electrostatic force field at either the haem or the flavin domain at neutral/alkaline pH values, and (iii) the introduction of alkaline residues (Lys, Arg) instead of neutral residues (Hydrophobic or hydrophilic) to increase the number of positive charges and weaken the negative electrostatic force field at neutral/alkaline pH.

[0030] Particularly the modification may be an increase of positive charge in the of amino acids 172-203 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1, preferably of amino acid 181, in particular preferred a D181K mutation, and/or a decrease of a negative charge of amino acids 565-577 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1, preferably of amino acid(s) 568 and/or 571, in particular preferred a D568S and/or E571S mutation, or any combination thereof.

[0031] In further embodiments the activity of the inventive CDH is a glucose dehydrogenase activity and may be an electrocatalytic oxidation of glucose.

[0032] The inventive CDH may be isolated, in particular from *C*hae*tomium atrobrunneum, Corynascus thermophilus, Hypoxylon* haema*tostroma, Neurospora crassa* or *Stachybotris bisbyi* or any genetically modified cell to recombinantly express the inventive CDH. Isolation may be performed by diafiltration and subsequent ion exchange chromatography by collecting fractions with CDH activity. The CDH can be further purified, e.g. using hydrophobic interaction chromatography.

[0033] The inventive CDH may also comprise a linker or be a part of a fusion protein. An inventive CDH polypeptide comprising the inventive sequences may be up to 500 kDa, up to 400 kDa, up to 300 kDa, up to 200 kDa or even up to 150 kDa.

[0034] In another aspect the present invention provides a nucleic acid molecule encoding a CDH of the invention. A

preferred embodiment of the invention is a nucleic acid molecule encoding a cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above and comprising

- a nucleotide sequence of SEQ ID NOs 4, 6, 8, 10 or 12, or
- the open reading frame of SEQ ID NOs 4, 6, 8, 10 or 12 or
- a nucleotide sequence with at least 50%, preferably at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identity to SEQ ID NO: 2, 4, 6, 8, 10 or 12 or the open reading frame of SEQ ID NOs: 2, 4, 6, 8, 10 or 12, further comprising a nucleotide mutation, substitution, deletion or insertion, preferably a codon mutation, substitution, deletion or insertion,
- a nucleotide sequence that hybridizes with any one of SEQ

[0035] ID NO: 2, 4, 6, 8, 10 or 12 under stringent condition. "Stringent conditions" relate to hybridisation reactions under defined hybridisation conditions which is a function of factors as concentration of salt or formamide in the hybridisation buffer, the temperature of the hybridisation and the post-hybridisation wash conditions. Such conditions are for example hybridisation at 68°C in a standard SSC hybridisation buffer containing 0.1%SDS followed by stringent washing in wash buffer at the same temperature. Stringent washing can be performed for example by two times washing with 2xSSC buffer followed by two wash steps with 0.5xSSC buffer. Stringent hybridisation conditions will preferably involve a temperature of 15°C to 25°C below the melting temperature (Tm), whereby the Tm of a hybridisation product of a nucleic acid probe can be calculated using a formula based on the g + c contained in the nucleic acids and that takes chain lengths into account, such as the formula Tm = 81.5 to 16.6 (log [na^+]) + 0.41 (% G + C) - 600/N), wherein N = chain length (Sambrook et al. (1989), which is incorporated herein by reference). In practice an estimated Tm for an oligonucleotide probe is often confirmed and thus a person skilled in the art can calculate the Tm for any chosen probe whose nucleotide sequence is known.

[0036] A nucleic acid sequence of *M. thermophilum* may be defined by the SEQ ID NO: 2 or the open reading frame of SEQ ID NO: 2, including homologs with at least 50%, preferably at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identity to SEQ ID NO: 2 or the open reading frame of SEQ ID NO: 2, further comprising a codon mutation, substitution, deletion or insertion to encode a CDH with glucose oxidation activity at a pH of 7.4 or above, preferably of amino acids 22 to 828 of SEQ ID NO: 1 with an additional amino acid substitution, deletion or insertion. Preferably the encoded CDH is of the amino acid sequence with the above mentioned amino acid modification.

[0037] The inventive nucleic acid molecules encoding a CDH with glucose oxidating activity at pH 7.4 may be isolated or purified. The inventive nucleic acid molecules, in particular their open reading frame may be comprised in a vector, preferably an expression or cloning vector. An inventive nucleotide molecule might further contain regulatory elements such as promotors and enhancers. Such a nucleic acid molecule comprising the inventive sequences may consist of up to 1,000,000 nucleotides, up to 900,000 nucleotides, up to 800,000 nucleotides, up to 700,000 nucleotides, up to 600,000 nucleotides, up to 500,000 nucleotides, up to 400,000 nucleotides, up to 300,000 nucleotides, up to 200,000 nucleotides, up to 100,000 nucleotides, up to 50,000 nucleotides or up to 25,000 nucleotides.

[0038] Particular benefits of the inventive CDHs are i) a high glucose turnover rate, ii) sufficient activity of the flavin domain and IET at pH 7.4 and iii) good DET characteristics. It was further found that these CDHs and other known CDHs are in particular suitable as anodic material in a bioelectrode as e.g. biosensor or biofuel cell.

[0039] One approach was to identify CDHs of different fungal strains from the phylum of ascomycota. It was found that some CDHs, e.g. from *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa* or *Stachybotris bisbyi* are able to convert glucose with high turnover rates at pH 7.4 and have additionally very good DET properties. Some of the found CDHs are new *per* se as mentioned above. A further aspect of the present invention is the use of all CDHs described herein on an electrode, in an electrochemical cell, in particular in a biosensor to measure glucose, preferably at a physiological pH such as pH 7.4.

[0040] Furthermore it was found that CDH from *M. thermophilum,* which is known to oxidise glucose and have good DET properties but shows no IET at pH values above pH 7.0, can be genetically engineered to increase the pH range of the IET to more alkaline conditions by means of site-directed mutagenesis. These CDHs were particularly suitable for electrochemical devices.

[0041] Thus, in a further aspect the present invention provides an electrode comprising an immobilised CDH having glucose oxidation activity at a pH of 7.4 or above and having at least 10%, at least 12%, at least 14%, at least 16%, preferably at least 18%, at least 19%, in particular preferred at least 20%, at least 21%, or even at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29% or at least 30% glucose, lactose or cellobiose oxidising activity at a pH of 7.4 as compared to their maximal activity at a lower pH as determined by the cyt c assay. Preferably the immobilised CDH also has a glucose oxidation activity at a pH of 7.4 or above and having at least 10%, at least 12%, preferably at least 18%, at least 19%, in particular preferred at least 20%, at least 21%, or

even at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29% or at least 30%, glucose, lactose or cellobiose oxidising activity at a pH of 7.4 as compared to their maximal activity at a lower pH as determined by a 2,6-dichloroindophenol (DCIP) assay. An electrode is generally a conducting surface, e.g. suitable for an electro-chemical element.

[0042] The activity measurement by either the cyt c or DCIP assay can be readily facilitated in a model system. The CDH can be directly used with the substrate (glucose but also lactose or cellobiose) and a reoxidising agent being either cyt c for reoxidation at the haem domain or DCIP for reoxidation at the flavin domain. The CDH is tested at a pH of 7.4 in any suitable buffer, e.g. a potassium or natrium phosphate buffer. To determine the maximum of the CDH activity, the activity is continuously measured at different pH values, e.g. ranging from pH 3 to pH 7.4 or higher and determining the maximum activity. The pH of 7.4 is then compared with this maximum activity and should have the required activity fraction mentioned above. The activity can e.g. be given as absolute values in U/mg or as relative values. Preferably, the inventive CDH has the required activity portion as compared to the maximum activity in both a cyt c and a DCIP assay. These activity values preferably also apply to the new CDHs described above, as such, independent of their fixation on an electrode. Preferably, the assay to determine the inventive CDH on the electrode is performed by glucose oxidation. Alternatively, also using lactose is possible.

[0043] The electrode may be of any material suitable to immobilise the CDH, e.g. carbon such as graphite, glassy carbon, boron doped diamond, gold electrodes modified with promoters e.g., thiols, screen-printed electrodes, screen printed electrodes containing carbon nanotubes (single or multi-walled). It may contain other nanoparticles to increase the specific surface area. Particular uses of the inventive electrodes are in the provision of biosensors and enzymatic biofuel cells, more specifically to glucose biosensors and glucose oxidizing biofuel cell anodes using the direct electron transfer properties (DET) of cellobiose dehydrogenase (CDH) to measure the glucose concentration at neutral, alkaline or, preferentially, physiological pH (in human body fluids, e.g., 7.4 in blood) or use glucose for the generation of an electric current in biofuel cells under the same pH conditions.

[0044] In particular preferred embodiments the specific activity for glucose oxidation by using the cyt c assay at pH 7.4 is higher than 0.5 U/mg, preferably at least 0.6 U/mg, at least 0.7 U/mg, at least 0.8 U/mg, at least 0.9 U/mg, at least 1 U/mg, or at least 1.2 U/mg CDH, or a current density higher than 80 nA/cm^2 at pH 7.4.

[0045] In further preferred embodiments the apparent K_M value of the CDH for glucose in solution (DCIP assays at optimum activity) is lower than 1.7 M, preferably lower than 1.5, lower than 1.2, preferably lower than 1 M or, when measured on electrodes an apparent K_M value below 200 mM, preferably below 150 mM.

[0046] In another embodiment the present invention provides an electrode, wherein the CDH is of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa* or *Stachybotris bisbyi* or a modified CDH of *Myriococcum thermophilum* with an increased activity at pH of 7.4 as defined in above, or homologues with certain sequence identities, amino acid modifications, etc. as defined above.

[0047] On the electrode, the CDH may be immobilised by adsorption, preferably also physical entrapment, complex formation, preferably via an additional complexing linker, covalent binding, in particular cross linking, or ionic linkage and/or the immobilized cellobiose dehydrogenase can be cross-linked, in particular by bifunctional agents, to increase stability or activity. It has been shown that crosslinking with bifunctional agents, such as agents with two reactive groups making a connection with the CDH, can stabilize the CDH and even increase its activity (measurable e.g. by the cyt c assay described herein). This advantage can lead to a increased sensitivity and lowering the detection limit for glucose. Such a cross-linking agent is e.g. glutaraldehyde or any other dialdehydes.

[0048] The electrodes might be used in form of a single electrode or electrode stacks. More specifically, the application of these enzymes is in (bio)electrochemical devices such as glucose biosensors or biofuel cells anodes. The electrode may be used as biosensor or as biofuel cell anode.

[0049] In another aspect the present invention provides an electro-chemical cell comprising an electrode as described above as an anodic element and a cathodic element.

[0050] In preferred embodiments of the electrochemical cell the anodic fluid can be glucose containing solution. Preferably the electrode is suitable for measurement in blood, serum and other body fluids.

[0051] The electrochemical cell may further comprise a solution of at least pH 6.0, preferably at least pH 6.5 or at least pH 6.7, in particular preferred at least pH 7.0, even more preferred at least pH 7.1, or at least pH 7.2, or at least pH 7.3, especially preferred at least 7.4, as anodic fluid.

[0052] According to another aspect a method of detecting or quantifying glucose in a sample is provided comprising

- providing a CDH having glucose oxidation activity at a pH of 7.4 or above,
- contacting a fluid sample having a pH of at least 6.0, preferably at least 6.5, or at least 6.7, more preferred at least 7.0, at least 7.1, at least 7.2, in particular preferred at least 7.3, especially preferred at least 7.4, with the CDH, and
- detecting an oxidation of glucose of the sample by the CDH.

[0053] Preferably the oxidation is detected electrochemically, preferably with an immobilised CDH on an electrode,

in particular preferred as defined above.

[0054] One of the world-wide leading causes of death and disability is diabetes. The diagnosis and management of diabetes mellitus requires continuous monitoring of blood glucose levels. Amperometric enzyme electrodes, based on glucose oxidase, play an increasingly important role and have been a target of substantial research. Most sensors are used for individual, daily diabetes monitoring, but the demand for continuous in vivo monitoring of patients is also significant. Real-time measurements are highly desired in intensive care units, during surgery, or for the management of diabetes, where rapid biochemical changes can be missed by discrete measurements. Such monitoring requires miniaturized, biocompatible, and stable sensors. Although research has reached the level of short-term implantation, an implantable glucose sensor possessing long-term stability has not yet been realised. Besides the obvious biocompatability challenge, some sensors are prone to errors due to low oxygen tension or electroactive interferences. Third generation biosensors depend on enzymes that are able to permit direct electron transfer (DET) between the electrode material and the redox active centre. Usually this is hindered by the encapsulation of the redox center by the protein structure. However, as has been shown herein, the inventive CDH can exhibit electrical communication with electrode supports.

[0055] In certain embodiments the CDH has at least 10%, or at least 12%, preferably at least 14%, or at least 16%, in particular preferred at least 18%, or at least 20%, at least 21%, or even at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29%, or at least 30%, glucose, lactose or cellobiose oxidising activity at a pH of 7.4 as compared to the maximal activity at a pH below 7.4 as determined by a cyt c assay and/or DCIP assay.

[0056] The fluid sample may be any fluid which potentially comprises glucose, including blood, serum and other body fluids.

[0057] In particularly preferred embodiments the CDH is of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon* haema*tostroma, Neurospora crassa* or *Stachybotris bisbyi* or a modified CDH of *Myriococcum thermophilum* with an increased activity at pH of 7.4 as defined above.

[0058] The cellobiose dehydrogenase of the present invention may be obtained from microorganisms of any genus. For purposes of the present invention the term "obtained from" as used herein in connection with a given source shall mean that the enzyme is produced by the source or by a cell in which the nucleic acid sequence of the cellobiose dehydrogenase gene from the source has been inserted. The enzyme or its nucleic acid sequence may be obtained from any fungal source and in a preferred embodiment from the genus *Chaetomium, Corynascus, Hypoxylon, Myriococcum, Neurospora* or *Stachybotrys*. In a more preferred embodiment the enzymes or the nucleic acid sequences are obtained from the species *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Myriococcum thermophilum, Neurospora crassa* or *Stachybotrys bisbyi.*

[0059] In the most preferred embodiment the enzymes or the nucleic acid sequences are obtained from the strains *Chaetomium atrobrunneum* CBS 238.71, *Corynascus thermophilus* CBS 405.69, *Hypoxylon haematostroma* CBS 255.63, *Myriococcum thermophilum* CBS 208.89, *Neurospora crassa* DSMZ 2968 or *Stachybotrys bisbyi* DSMZ 63042.

[0060] It will be understood that for the aforementioned species, the invention encompasses both the perfect and imperfect states and other taxonomic equivalents, e.g., anamorphs, regardless the species name by which they are known. Those skilled in the art will readily recognise the identity of appropriate equivalents.

[0061] It is understood that one of skills in the art may engineer the mentioned or other cellobiose dehydrogenases to obtain the outlined specifications of the enzymes and enzyme variants described herein to obtain modified enzymes using the principles outlined herein like the rational approach via site-directed mutagenesis or directed evolution approaches (e.g., gene shuffling, error-prone PCR) and subsequent screening of the generated diversity. The techniques to introduce a mutation into the nucleic acid sequence to exchange one nucleotide for another nucleotide with the aim to exchange one amino acid for another in the resulting protein may be accomplished by site-directed mutagenesis using any of the methods known in the art.

[0062] Preferably the present invention is defined as follows:

Definition 1. A CDH having glucose oxidation activity at a pH of 7.4 or above, selected from an CDH isolated from *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa* or *Stachybotris bisbyi* or being a modified CDH of *Myriococcum thermophilum,* e.g. selected from the group of a CDH of *Chaetomium atrobrunneum, Hypoxylon haematostroma, Stachybotris bisbyi* or a modified CDH of *Myriococcum thermophilum.*

Definition 2. Cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprising an amino acid sequence of SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11.

Definition 3. Cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprising an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11.

Definition 4. CDH according to definition 1 being a modified CDH of *Myriococcum thermophilum,* comprising a flavin

and a haem domain, wherein electron transfer from the flavin to the haem domain is increased as compared to wild type CDH of *Myriococcum thermophilum,* preferably as measured by a cyt c assay.

Definition 5. CDH having glucose oxidation activity at a pH of 7.4 or above comprising an amino acid sequence of amino acids 22 to 828 of SEQ ID NO: 1 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to amino acids 22 to 828 of SEQ ID NO: 1, characterised in that the amino acid sequence has at least one additional amino acid substitution, deletion or insertion to the sequence of SEQ ID NO:1 increasing electron transfer from the flavin to the haem domain as compared to wild-type CDH of *M. thermophilum* of SEQ ID NO:1, preferably as measured by a cyt c oxidation assay.

Definition 6. CDH according to definition 4 or 5, **characterised in that** the electron transfer is increased by increasing , preferably optimising, electrostatic interactions between the flavin and the haem domain.

Definition 7. CDH according to any one of definition 4 to 6, **characterised in that** the modification is a modification of the haem domain of any one of amino acids 90-100, 115-124, 172-203, preferably of any one of amino acids 176, 179-182, 195, 196, 198, 201 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1 and/or of the flavin domain of any one of amino acids 311-333, 565-577, 623-625, 653-664, 696-723, preferably of any one of amino acids 318, 325, 326, 328, 568, 571, 574, 575, 624, 654, 663, 702, 709, 712, 717, correspond to the *M. thermophilum* CDH of SEQ ID NO: 1, or any combination thereof.

Definition 8. CDH according to definition 7, **characterised in that** the modification is an increase of positive charge in the of amino acids 172-203 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1, preferably of amino acid 181, in particular preferred a D181K mutation, and/or a decrease of a negative charge of amino acids 565-577 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1, preferably of amino acid(s) 568 and/or 571, in particular preferred a D568S and/or E571S mutation, or any combination thereof.

Definition 9. CDH according to any one of definition 1 to 8, **characterised in that** the glucose oxidation activity is a glucose dehydrogenase activity.

Definition 10. CDH according to any one of definition 1 to 9, **characterised in that** the activity is an electrocatalytic oxidation of glucose.

Definition 11. CDH according to any one of definition 1 to 10, being isolated by diafiltration, ion exchange chromatography by collecting fractions with CDH activity, preferably being further purified by hydrophobic interaction chromatography.

Definition 12. A nucleic acid molecule encoding a cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above and comprising

- a nucleotide sequence of SEQ ID NOs 4, 6, 8, 10 or 12, or
- the open reading frame of SEQ ID NOs 4, 6, 8, 10 or 12 or
- a nucleotide sequence with at least 50%, preferably at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identity to SEQ ID NO: 2, 4, 6, 8, 10 or 12 or the open reading frame of SEQ ID NOs: 2, 4, 6, 8, 10 or 12, further comprising a nucleotide mutation, substitution, deletion or insertion, preferably a codon mutation, substitution, deletion or insertion,
- a nucleotide sequence that hybridizes with any one of SEQ ID NO: 2, 4, 6, 8, 10 or 12 under stringent condition, preferably encoding a cellobiose dehydrogenase as defined in any one of definition 1 to 11.

Definition 13. An electrode comprising an immobilised CDH having glucose oxidation activity at a pH of 7.4 or above and having at least 10%, preferably at least 14%, in particular preferred at least 18%, or at least 20%, at least 21%, or even at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29%, or at least 30%, glucose, lactose or cellobiose oxidising activity at a pH of 7.4 as compared to their maximal activity at a lower pH as determined by the cyt c assay, preferably also as compared to their maximal activity at a lower pH as determined by the DCIP assay, and/or an electrode comprising an immobilised CDH of any one of definitions 1 to 11.

Definition 14. Electrode according to definition 13, characterised in that the cyt c assay is performed by cellobiose oxidation.

Definition 15. Electrode according to definition 13 or 14, characterised in that the glucose oxidation activity at pH 7.4 is at least 0.5 U/mg CDH.

Definition 16. Electrode according to any one of definition 13 to 15, **characterised in that** the Km value of the CDH for an glucose oxidation reaction at pH 7.4 is below 1M.

Definition 17. Electrode according to any one of definition 13 to 16, **characterised in that** the CDH is of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa, Stachybotrys bisbyi,* or a modified CDH of *Myriococcum thermophilum* with an increased activity at pH of 7.4 as defined in any one of definition 4 to 8, or

the cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprises an amino acid sequence of SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11,
preferably the CDH is further defined as in any one of definition 1 to 11.
Definition 18. Electrode according to any one of definition 13 to 16, **characterised in that** the CDH is immobilised by adsorption, complex formation, preferably via an additional complexing linker, covalent or ionic linkage, and/or wherein the immobilized cellobiose dehydrogenase is cross-linked, in particular by bifunctional agents, to increase stability or activity. Definition 19. An electrochemical cell comprising an electrode according to any one of definition 13 to 18 as an anodic element and a cathodic element.
Definition 20. Electrochemical cell according to definition 19, comprising a glucose containing solution as anodic fluid. Definition 21. Electrochemical cell according to definition 18 or 20, comprising a solution of at least pH 6.0, preferably at least pH 6.5, in particular preferred at least pH 7.0, even more preferred at least pH 7.2, as anodic fluid.
Definition 22. Method of detecting or quantifying glucose in a sample using any of the previously described CDHs or electrodes or the method comprising

- providing a CDH having glucose oxidation activity at a pH of 7.4 or above,
- contacting a fluid sample having a pH of at least 6.5, preferably at least 7.0, in particular preferred at least 7.3, especially preferred at least 7.4, with the CDH, and
- detecting an oxidation of glucose of the sample by the CDH.

Definition 23. Method according to definition 22, wherein the oxidation is detected electrochemically, preferably with an immobilised CDH on an electrode, in particular preferred as defined in any one of definition 13 to 21.
Definition 24. The method of definition 22 or 23, **characterised in that** the CDH has at least 10%, preferably at least 14%, in particular preferred at least 18%, or at least 20%, at least 21%, or even at least 22%, at least 23%, at least 24%, at least 25%, at least 26%, at least 27%, at least 28%, at least 29%, or at least 30%, glucose, lactose or cellobiose oxidising activity at a pH of 7.4 as compared to the maximal activity at a pH below 7.4 as determined by a cyt c assay.
Definition 25. The method of definition 22 to 24, **characterised in that** the CDH is of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa* or *Stachybotris bisbyi* or a modified CDH of *Myriococcum thermophilum* with an increased activity at pH of 7.4 as defined in any one of definition 4 to 8, preferably the CDH is further defined as in any one of definition 1 to 11.
Definition 26. The method of any one of claims 22 to 25, characterized in that the cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprises an amino acid sequence of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11.

[0063] The present invention is further illustrated by the following figures and examples without being restricted thereto.

Figure:

[0064]

Figure 1 gives the codon-optimised nucleotide sequence (SEQ ID NO: 2) and the corresponding amino acid sequence (SEQ ID NO: 1) of *Myriococcum thermophilum* CDH used for site-directed mutagenesis. Non-limiting preferred mutations sites are indicated by "*" and particular non-limiting preferred sites are marked by "+".

Figure 2 shows the pH profiles of screened ascomycete CDHs *Chaetomium atrobrunneum* CDH, 2.a; *Corynascus thermophilus* CDH, 2.b; *Hypoxylon haematostroma* CDH, 2.c; *Neurospora crassa* CDH, 2.d; *Stachybotrys bisbyi* CDH, 2.e; *Myriococcum thermophilum* CDH, 2.f; and the genetically engineered enzyme variants *Myriococcum thermophilum* CDH variant D160K, 2.g; *Myriococcum thermophilum* CDH variant D547S/E550S, 2.h using lactose and a soluble electron acceptor, 2,6-dichloroindophenol, (DCIP, dotted, grey lines) or cyt c (solid, black lines) as substrates and 50 mM citrate-phosphate buffer (pH 3.0-8.0).

Figure 3 is a sequence alignment of amino acid sequences of CDHs from *Chaetomium atrobrunneum* (SEQ ID NO: 5), *Corynascus thermophilum* (SEQ ID NO: 7), *Hypoxylon haematostroma* (SEQ ID NO: *3), Myriococcum thermophilum* (SEQ ID NO: 1), *Neurospora crassa* (SEQ ID NO: 11) and *Stachybotrys bisbyi* (SEQ ID NO: 9).

Figure 4 shows a setup of the wall jet electrode and auxiliary instruments. The sensor assembly (A) was continuously flushed with buffer and samples were applied through an ultrafast injection valve. The obtained current at a potential of 300 mV was recorded. The flow-jet system (A) consisted of a carbon working electrode (WE), a platin counter electrode (CE) and a silver reference electrode (RE) connected to a potentiostat.

Figure 5: Measurement setup of the flow-cell system

Examples:

Example 1: Materials

[0065] Chemicals used in buffers and fermentation media were commercial products and at least of analytical grade if not otherwise stated. Peptone from meat and microcrystalline cellulose were from VWR International (Vienna, Austria), alpha-cellulose from Sigma-Aldrich (Vienna, Austria). Substrates for kinetic studies were lactose, glucose, 2,6-dichloroindophenol (DCIP) and cytochrome c from horse heart(cyt c) from Sigma-Aldrich in the highest grade of purity available. Buffers were prepared using water purified and deionised (18 MΩ) with a Milli-Q system (Millipore, Bedford, MA, USA), fermentation media contained reversed osmosis water (0.1 MΩ).

Example 2: Enzyme Assays

[0066] Enzymatic activity of cellobiose dehydrogenase was detected by two assays. The DCIP assay, measuring the activity of the flavin domain was performed by measuring the time-dependent reduction of 300 μM DCIP in 50 mM citrate-phosphate buffer at the indicated pH (3.0-8.0), containing 30 mM lactose at 520 nm and 30 °C. The absorption coefficient for DCIP is pH dependent but differs at 520 nm only about 3% within pH 3.0 to 8.0 and was determined to be 6.8 mM^{-1} cm^{-1} (Karapetyan et al., 2005 Journal of Biotechnology 121: 34-48).

[0067] Alternatively, enzymatic activity was determined by the reduction of cytochrome *c* at 30°C and 550 nm (cyt *c*, ε_{550} = 19.6 mM^{-1} cm^{-1}, Canevascini et al., 1991, European Journal of Biochemistry 198: 43-52) in an assay containing 20 μM cyt *c* and 30 mM lactose, which specifically detects the activity of the whole enzyme (flavin and haem domain). The cyt *c* assay gives thereby also a measure of the efficiency of the intramolecular electron transfer (IET) between both domains as an indication of the enzyme's response on electrodes in a pH range of 3.0 to 8.0 (50 mM sodium citrate-phosphate buffer). For the detection of activity with glucose the above mentioned assays were used, but lactose was exchanged for 100 mM glucose.

[0068] One unit of enzymatic activity was defined as the amount of enzyme that oxidises 1 μmol of lactose per min under the assay conditions. Lactose was chosen instead of the natural substrate cellobiose, as it shows no substrate inhibition with CDH. The reaction stoichiometry with carbohydrates is 1 for the two-electron acceptor DCIP, but 2 for the one-electron acceptor cyt *c*.

Example 3: Enzyme Kinetics

[0069] Carbohydrate stock solutions used for measuring activity and kinetic constants with the DCIP and cyt *c* assays were prepared in the appropriate buffer several hours before the experiment to allow mutarotation to reach equilibrium. pH profiles were determined using 50 mM citrate-phosphate buffer (3.0-8.0). To ensure an assay temperature of 30 °C the cuvettes were incubated in a thermostated chamber for at least 20 min. After the measurement, the pH was again checked in the cuvettes. Kinetic constants were calculated by fitting the observed data to the Henri-Michaelis-Menten equation or to the adapted model for substrate inhibition using nonlinear least-squares regression and the program SigmaPlot (Systat Software, San Jose, CF, USA).

Example 4: Protein characterisation

[0070] The protein concentration was determined by the dye-staining method of Bradford using a pre-fabricated assay from Bio-Rad Laboratories Hercules, CA, USA) and bovine serum albumin as standard according to the manufacturers recommendations.

[0071] For spectral characterisation apparently homogeneous CDH (in the oxidised state) was diluted to an absorption of ~1 at 280 nm and the spectrum from 260 to 700 nm taken with an Hitachi U3000 spectrophotometer (Tokyo, Japan). After reduction with lactose (final concentration 1 mM) the reduced spectrum was taken.

[0072] For electrophoretic characterisation SDS-PAGE was carried out on a Hoefer SE 260 Mighty Small II vertical electrophoresis unit. Gels (10.5x10 cm; 10% T, 2.7% C) were cast and run according to the manufacturers' modifications of the Laemmli system. Isoelectric focusing in the range of pH 2.5 to 6.5 was performed on a Multiphor II system using

precast, dry gels rehydrated with Ampholytes (GE Healthcare Biosiences, Vienna, Austria). Protein bands on the SDS-PAGE were stained with silver, bands on the IEF gel with Coomassie blue R-250, according to the instructions.

Example 5: Screening for Suitable Cellobiose Dehydrogenases

[0073] Fungal strains (*Chaetomium atrobrunneum* CBS 238.71, Corynascus thermophilus CBS 405.69, *Hypoxylon haematostroma* CBS 255.63, *Myriococcum thermophilum* CBS 208.89, *Neurospora crassa* DSMZ 2968 and *Stachybotrys bisbyi* DSMZ 63042) were obtained from the Centraalbureau voor Schimmelcultures (CBS, Utrecht, The Netherlands) and Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ, Braunschweig, Germany) in freeze dried or actively growing form on agar slants and were periodically subcultured on potato dextrose agar (PDA) plates. Freshly inoculated agar plates were grown at 25 or 30 °C, depending on the published growth temperatures of the cultures until reaching a diameter of 5 cm and then used to inoculate shaking flasks. The medium used for submersed cultures contained (per litre): 20 g of alpha-cellulose, 5 g of peptone from meat and 0.3 ml of a trace element solution. The trace element solution contained (per litre) : 1 g of $ZnSO_4 \cdot 7H_2O$, 0.3 g of $MnCl_2 \cdot 4H_2O$, 3 g of H_3BO_3, 2 g of $CoCl_2 \cdot 6H_2O$, 0.1 g of $CuSO_4 \cdot 5H_2O$, 0.2 g of $NiCl_2 \cdot 6H_2O$, 4 ml of H_2SO_4 (Sachslehner et al., 1997, Applied Biochemistry and Biotechnology 6365: 189-201). For the cultivation in shaking flasks, 1 L Erlenmeyer flasks were filled with 0.3 L of medium. After sterilisation the flasks were inoculated with 3 cm^2 of finely cut mycelium from PDA plates and incubated in a rotary shaker (110 rpm, eccentricity = 1.25 cm) at 25 or 30 °C. Samples were taken regularly and the production of CDH was monitored.

Example 6: CDH Production and Purification from Fungal Sources

[0074] CDH production was performed in up to 16 parallel shaking flask cultures per strain using identical conditions as in the screening procedure. Cultures were harvested on the day exhibiting maximum cyt c activity. The culture supernatant was separated from residual cellulose and fungal biomass by centrifugation (20 min, 6000 x g) and concentrated and diafiltrated using a polyethersulfone hollow fibre cross-flow module with a 10 kDa cut-off (Microza UF module SLP-1053, Pall Corporation) until a conductivity of 2 mS cm^{-1} was reached. The concentrated enzyme preparation was applied to a DEAE Sepharose column (chromatography equipment from GE Healthcare Biosciences) mounted on an ÄKTA Explorer system and equilibrated with 50 mM sodium acetate buffer, pH 5.5. The column was eluted with a linear salt gradient (0 to 0.5 M NaCl in the same buffer) in 10 column volumes (CV). Fractions with a high specific CDH activity were pooled, saturated ammonium sulphate solution was slowly added at 4 °C to 20% final saturation and applied to a PHE-Source column equilibrated with 100 mM sodium acetate buffer, pH 5.5 containing $(NH_4)_2SO_4$ (20% saturation) and 0.2 M NaCl. The column was eluted with a linear gradient (0 to 100% of 20 mM sodium acetate buffer, pH 5.5) in 10 CV. The purest CDH fractions were pooled, desalted with 20 mM sodium acetate buffer, pH 5.5, concentrated and frozen at -70 °C for further use.

Example 7: Obtaining Nucleotide and Protein Sequences of New CDHs.

[0075] Mycelium for nucleic acid isolations was harvested from cellulose induced growing cultures after 5 days. The mycelium was frozen in liquid nitrogen and homogenized using mortar and pestle. Portions of 100 mg mycelium were used for DNA extraction (Liu et al., 2000, Journal of Clinical Microbiology, 38: 471). Total RNA was isolated using TriFast (Peqlab, Erlangen, Germany). cDNA synthesis was performed with the First Strand cDNA Synthesis Kit (Fermentas, Vilnius, Lithuania) and the anchor primer (5'-GGCCACGCGTCGACTAGTACTTTTTTTTTTTTT-3'). Degenerated primer on the basis of known ascomycete CDH sequences were used to amplify fragments of genomic DNA encoding for CDH. For the amplification of the adjacent upstream region the DNA Walking SpeedUp Premix Kit (Seegene, Seoul, Korea) was used. For the amplification of the 3' region cDNA was used as a template. To obtain full-length cDNA clones encoding the CDH proteins a nested PCR with two specific forward primer upstream of the putative start codon and two reverse primer, one specific for a sequence shortly downstream of the stop codon and the universal primer (5'-GTACTAGTCGACGCGTGGCC-3') complementary to the anchor primer, was done. Names in the following primer table are abbreviated as follows: *Chaetomium atrobrunneum,* CA; Corynascus thermophilus, CT; *Hypoxylon haematostroma,* HH; *Neurospora crassa,* NC; *Stachybotrys bisbyi,* SB.

	FORWARD PRIMER		REVERSE PRIMER
5'-HH-1	ATGCCTCTCTTGTTTGGACCG	UNIVERSAL	
5'-HH-2	TCAACTCTCATACTTGGCTTGG	3'-HH-1	TACATCCAGCTTACCGGCACTG
5'-CA-1	TAGAGTCGAGGCGAACCAG	UNIVERSAL	

(continued)

	FORWARD PRIMER		REVERSE PRIMER
5'-CA-2	TTGCTGCTGTGCTCCTATGC	3'-CA-1	TTCCTTCCCTCCATCAACTCC
5'-SB-1	TCTTGCTACGCACTTCGGTATTG	UNIVERSAL	
5'-SB-2	TGTGTACCCTGTTTACTCACC	3'-SB-1	GTACCCATTAAGTACACTGCCAG
5'-CT-1	TCTTATAAGCCTTTGGCTCC	UNIVERSAL	
5'-CT-2	TTGGCTCCGTTGGAACAATG	3'-CT-1	TTCCCCCTTCGAATTCGGTC
5'-NC-1	CGCACCAACCGTGTGAAGTG	UNIVERSAL	
5'-NC-2	TACAAGATGAGGACCACCTCG	3'-NC-1	AGCTACCTATCACCCTCTGTC

[0076] The obtained PCR products were then fully sequenced to obtain the complete nucleic acid sequence of the respective cdh gene.

Example 8: Generation of *Myriococcum thermophilum* CDH variants by site-directed mutagenesis

[0077] For enhanced production of recombinant *Myriococcum thermophilum* CDH (Zamocky et al., 2008,) in *Pichia pastoris* the gene (gene bank accession code EF 492052, GI:164597963) was codon optimised (**FIG 1**) for expression in P. *pastoris* and synthesized by GenScript (Piscataway, NJ, USA). The gene shows a maximum similarity with CDH from *Thielavia heterothallica* (74% identity) and only 63% identity with the gene from *Humicola insolens.* On the protein level, the similarity is highest to *Thielavia heterothallica* CDH (93% identity, 97% positives, 0% gaps) and quite low for *Humicola insolens* CDH (61 % identity, 71% positives, 2% gaps).

[0078] The synthetic *M. thermophilum* CDH gene was mutated by a two-step site-directed mutagenesis protocol using PCR and Dpn*I* digestion. The yeast vector pPICZ A carrying the synthetic CDH gene was used as template for mutagenic PCR. For the replacement of Asp160 with Lys the primers 5'-TCCAAGCTTTT**AAA**GATCCAGGTAAC-3' (Mt CDH-D160K-fw) and 5'-AAAAGCTTGGACCCAACCAAG-3' (Mt CDH-D160K-rv) were used. For the double mutant D547S/E550S primers 5'-GTCTTCTAT**TCT**TTTTAC**TCT**GCTTGGGATG -3' (Mt CDH- D547S/E550S -fw) and 5'- AT-AGAAGACCACATCAGGG -3' (Mt CDH- D547S/E550S -rv) were used. The mutation sites are indicated by bold letters in the mutagenic forward primers. PCR was performed under the following conditions: 98 °C for 30 s, then 32 cycles of 98 °C for 10 s; 62 °C for 20 s; 72 °C for 2 min, with a 10 min final extension at 72 °C. The 50 μl reaction mix contained Phusion HF Buffer (New England Biolabs, Ipswich, MA, USA), 0.1 μg of plasmid DNA, 1 unit of Phusion DNA polymerase (New England Biolabs), 10 μM of each dNTP and 5 pmol of each primer.

[0079] PCR reactions were separated by agarose gel electrophoresis and bands at 6 kB purified using the Wizard SV Gel and PCRClean-Up System (Promega, Madison, WI, USA). The purified PCR fragment was digested with DpnI (Fermentas, Vilnius, Lithuania) to remove methylated DNA. 10 μl of this reaction was used to transform chemically competent NEB-5-Alpha E. *coli* cells (New England Biolabs) according to the manufacturer. For each mutation 3 colonies were checked by sequencing for the presence of the correct mutation. The purified plasmid of a positive clone was linearized with *SacI* and used to transform competent X-33 *P. pastoris* cells. Colonies growing on YPD zeocin agar plates (100 mg/L) were checked by PCR for the integration of the construct. Two positive clones of each mutation were further cultivated under induced condition and analysed for CDH production. The clones with the highest yield were selected for fermentation.

Example 9: Production of recombinant CDH

[0080] An overnight pre-culture of a *Pichia pastoris* transformant (selected from a YPD plate with 100 mg/L Zeocin) was inoculated into 0.3 L of production stage medium in a Infors HT multifermenter (Bottmingen, Switzerland). The production stage medium contained per litre: 26.7 ml of H_3PO_4 (85%); 0.93 g of $CaSO_4 \cdot 2H_2O$; 14.9 g of $MgSO_4 \cdot 7H_2O$; 18.2 g of K_2SO_4; 4.13 g of KOH; 4% (v/v) glycerol; 1.45 ml of PTM_1 trace element solution for P. *pastoris* according to the Invitrogen manual 053002 Ver. B (Carlsbad, CF, USA). The PTM_1 trace element solution contains per litre: 6 g of $CuSO_4 \cdot 5H_2O$, 0.08 g of NaI, 3 g of $MnSO_4 \cdot H_2O$, 0.2 g of $NaMoO_4 \cdot 2H_2O$, 0.02 g of H_3BO_3, 0.5 g of $CoCl_2$, 20 g of $ZnCl_2$, $FeSO_4 \cdot 7H_2O$, 0.2 g of biotin, 5 ml of sulfuric acid. A glycerol feed was performed with an addition of 9 $gL^{-1}h^{-1}$ until the wet cell weight exceeded 150 g per litre. As soon as the residual glycerol was used up (determined by monitoring the increase of the dissolved oxygen tension), a methanol feed (100% methanol containing 12 ml PTM_1 trace element solution per litre) with an average addition of 3 $gL^{-1}h^{-1}$ was started and continued for 72 h at 30 °C and 20% oxygen

tension. The culture supernatant was separated from residual biomass by centrifugation (20 min, 6000 x g) and concentrated and purified by hydrophobic interaction chromatography. To that purpose, saturated ammonium sulphate solution was slowly added to the clear culture supernatant at 4 °C to 20% final saturation. After a second centrifugation step (30 min, 30,000 x g) the solution was applied to a PHE-Source column (GE Healthcare Biosciences) equilibrated with 100 mM sodium acetate buffer, pH 5.5 containing $(NH_4)_2SO_4$ (20% saturation) and 0.2 M NaCl. The column was eluted with a linear gradient (0 to 100% of 20 mM sodium acetate buffer, pH 5.5) in 10 CV. The purest CDH fractions were pooled, desalted with 20 mM sodium acetate buffer, pH 5.5, concentrated and stored for further use.

Example 10: Electrochemical Equipment

[0081] A three electrode flow through amperometric wall jet cell was used (Appelqvist et al, Anal. Chim. Acta, 169 (1985) 237-47.*)* and contained the working electrode (graphite electrode modified with CDH), a reference electrode (Ag|AgCl in 0.1 M KCl) and a counter electrode made of a platinum wire, connected to a potentiostat (Zäta Elektronik, Höör, Sweden). The enzyme modified electrode was pressfitted into a Teflon holder and inserted into the wall jet cell and kept at a constant distance (ca. 1 mm) from the inlet nozzle. The response currents were recorded on a strip chart recorder (Kipp & Zonen, Delft, The Netherlands). The electrochemical cell was connected on-line to a single line flow injection (FI) system, in which the carrier flow was maintained at a constant flow rate of 0.5 ml min^{-1} by a peristaltic pump (Gilson, Villier-le-Bel, France). The injector was an electrically controlled six-port valve (Rheodyne, Cotati, CA, USA), and the injection loop volume was 50 μl.

[0082] For the screen-printed electrodes a special methacrylate wall jet flow for flow injection analysis (FIA) from DropSense (Oviedo, Spain) was used. The electrochemical cell consists of a carbon working electrode (4 mm diameter), a carbon counter electrode and silver reference electrode connected to a potentiostat (Zäta Elektronic). The response currents were recorded on a strip chart recorder (Kipp & Zonen). The electrochemical cell was connected on-line to a single flow injection (FI) system, in which the carrier flow was maintained at a constant flow rate of 0.5 ml min^{-1} by a peristaltic pump (Gilson). For injection an electronically controlled six-port valve (Rheodyne) and a injection loop (50 μl) was used.

Example 11: Preparation of Enzyme Modified Graphite Electrodes

[0083] CDH was immobilised through simple chemo-physical adsorption onto the surface of solid spectroscopic graphite electrodes (diameter = 3.05 mm, Ringsdorff Spektralkohlestäbe, SGL Carbon Sigri Greatlakes Carbon Group Ringsdorff-Werke GmbH, Bonn Germany). The electrode was cut and polished on wet emery paper (Tufbak, Durite, P400) and afterwards carefully rinsed with Milli-Q water and dried. Then 5 μl of enzyme solution was spread onto the entire active surface of the electrode (0.0731 cm^2). The electrode was dried at room temperature and then stored overnight at 4 °C. Before use, the electrode was thoroughly rinsed with Milli-Q water in order to remove any weakly adsorbed enzyme and plugged into in the wall jet cell already containing buffer. Then, the required potential was applied until a stable background current was obtained before any substrate was injected into the flow system.

Example 12: Preparation of Enzyme-Modified Screen Printed Electrodes

[0084] Five μl of enzyme solution was placed on the carbon-based electrode (DropSens, Oviedo, Spain) so that the whole area was entirely coated with solution. The immobilisation was allowed to proceed overnight at 4°C. Before use the electrodes were thoroughly rinsed with water. Cross-linking of the biocomponent was carried out by chemical modification with glutaraldehyde where 1 μl of an aqueous 1% glutaraldehyde solution was applied on the enzyme layer at 37°C for 10-15 min. After rinsing the electrodes were allowed to dry at room temperature.

[0085] The optimum for the applied potential was determined with a 10 mM lactose solution. The potential was varied stepwise from - 250 to +600 mV vs. Ag|AgCl in 0.1 M KCl and +300 mV chosen for further experiments.

Example 13: pH Profiles of CDH Immobilised on Electrodes

[0086] The activity versus pH-profile for direct electron transfer (DET) of the adsorbed enzyme was determined electrochemically using a flow injection system. The substrate was lactose with a concentration of 5 mM. As enzyme assays should proceed under saturating substrate conditions so that slight variations in the absolute concentration have no influence on the reaction rate an amount at least 10 times the K_M-value should be present. The following buffers were used in the experiments: 50 mM sodium citrate buffer (pH 3.0-6.5), 50 mM sodium phosphate buffer (pH 6.0-9.0). The buffers were degassed before use to prevent micro bubbles in the flow system.

Example 14: Heterogeneous Enzyme Kinetics on Electrodes

[0087] The kinetic parameters K_M (Michaelis-Menten constant) and V_{max} (maximum volumetric activity), in this case equal to I_{max} (maximum response in current), were determined for a number of substrates in the DET mode (the electron acceptor being the graphite electrode). All kinetic parameters were calculated by nonlinear least-square regression, fitting the observed data to the Henri-Michaelis-Menten equation. These calculations were done after correcting the substrate concentration values using the dispersion factor of the flow system used including the wall jet cell by dividing the steady state current registered for a 50 mM ferrocyanide solution with that of the peak current for the injected sample having an equal concentration of ferrocyanide and using an applied potential of 400 mV (Ruzicka and Hansen, Flow Injection Analysis, 2nd ed., Wiley, New York 1988). In our case, for a 1 mm distance between electrode and inlet nozzle and 0.5 ml min^{-1} flow rate, the dispersion factor D was equal to 1.18 (Fig. 5).

Example 15: CDH of *Chaetomium atrobrunneum*

[0088] A cellobiose dehydrogenase with high glucose turnover rates and activity under physiological pH conditions was obtained from liquid cultures of *Chaetomium atrobrunneum.* The culture was grown and screened as described. The maximum activity under the chosen conditions was 90 U/L (cyt c assay, pH 6.0, 11^{th} day).For enzyme production and purification the outlined procedures were applied and resulted in an CDH preparation with a specific activity of 11.7 U/mg (DCIP assay, pH 6.0), an apparent molecular weight of 90 kDa as determined by SDS-PAGE and an isoelectric point of 4.6. The calculated molecular weight of the obtained protein sequence is 86.047 kDa and fits well to the native CDH. The calculated isoelectric point is 5.0. The spectrum of *Chaetomium atrobrunneum* CDH is typical and shows the haem alpha-, beta- and gamma-bands of the reduced enzyme at 563, 533 and 430 nm. In the oxidised enzyme the gamma-band has its absorption maximum at 421 nm with a shoulder at 450 nm, which disappears after reduction with lactose and corresponds to the absorption peak of the FAD cofactor. Kinetic characterisation with the cyt c assay and lactose as electron donor resulted in a neutral pH profile with an activity maximum at pH 5.0 and still 18% relative activity at pH 7.4 (**FIG 2.a**). The specific activity at pH 7.4 was 0.88 U/mg using the cyt c assay and glucose as substrate. The pH optimum of the flavin domain was obtained with the DCIP assay and shows a more acidic pH optimum, however, the flavin domain is sufficiently active at pH 7.4 also with this electron acceptor. Kinetic constants for glucose (obtained with the cyt c assay at pH 5.0) are a K_M of 240 mM and a k_{cat} of 17.5 s^{-1} for glucose, which shows in comparison to currently known enzymes a far better suitability of this enzyme for the proposed application.

[0089] To test the electrochemical behaviour of *Chaetomium atrobrunneum* CDH on electrodes, the purified enzyme preparation was immobilised by adsorption on a spectroscopic graphite electrode surface. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the current at pH 7.4. The optimum pH under the chosen conditions is 5.6 and 48% of the maximum current was obtained at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH on the electrode surface was determined to be 80 mM and I_{max} = 30 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 233 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 3-15 mM.

Example 16: CDH from Corynascus thermophilus

[0090] A cellobiose dehydrogenase with high glucose turnover rates and activity under physiological pH conditions was obtained from liquid cultures of *Corynascus thermophilus.* The culture was grown as described in (Gautsch, diploma thesis, Universität für Bodenkultur, Wien, 2004). The maximum activity obtained was 1400 U/L (cyt c assay, pH 6.0, 6^{th} day). For enzyme production and purification the outlined procedures were applied and resulted in a CDH preparation with a specific activity of 17.9 U/mg, an apparent molecular weight of 87 kDa as determined by SDS-PAGE and an isoelectric point of 4.1. The calculated molecular weight of the obtained protein sequence is 81.946 kDa and fits well to the native CDH. The calculated isoelectric point is 4.64. The spectrum of *C. thermophilus* CDH is typical and shows the haem α-, β- and γ-bands of the reduced enzyme at 562, 533 and 429 nm. In the oxidised enzyme the γ-band has its absorption maximum at 420 nm with a shoulder at 450 nm, which disappears after reduction with lactose and corresponds to the absorption peak of the FAD cofactor. Kinetic characterisation with the cyt c assay resulted in a pH profile with an activity maximum at pH 7.5 and 98% relative activity at pH 7.4 (**FIG 2.b**). The specific activity at pH 7.4 was 3.6 U/mg using the cyt c assay and glucose as substrate. The pH optimum of the flavin domain was obtained with the DCIP assay and shows a more acidic pH optimum, however, the flavin domain is sufficiently active at pH 7.4 also with this electron acceptor. Kinetic constants for glucose (obtained with the cyt c assay at pH 5.0) are a K_M of 950 mM and a k_{cat} of 32 s^{-1} for glucose.

[0091] To test the electrochemical behaviour of *C. thermophilus* CDH on electrodes, the purified enzyme preparation

was immobilised by adsorption on a spectroscopic graphite electrode surface. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the current at pH 7.4. The optimum pH under the chosen conditions is 8.5 and 96% of the maximum current was obtained at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH on the electrode surface was determined to be 188 mM and I_{max} = 190 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 3500 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 1-15 mM.

Example 17: CDH of *Hypoxylon haematostroma*

[0092] A cellobiose dehydrogenase with high glucose turnover rates and activity under physiological pH conditions was obtained from liquid cultures of *Hypoxylon haematostroma.* The culture was grown and screened as described. The maximum activity under the chosen conditions was 65 U/L (cyt c assay, pH 6.0, 9^{tn} day).For enzyme production and purification the outlined procedures were applied and resulted in an CDH preparation with a specific activity of 15.3 U/mg (DCIP assay, pH 6.0), an apparent molecular weight of 85 Da as determined by SDS-PAGE and an isoelectric point of 4.1. The calculated molecular weight of the obtained protein sequence is 87.514 kDa and fits well to the native CDH. The calculated isoelectric point is 6.37. The spectrum of *Hypoxylon haematostroma* CDH is typical and shows the haem alpha-, beta- and gamma-bands of the reduced enzyme at 563, 533 and 429 nm. In the oxidised enzyme the gamma-band has its absorption maximum at 421 nm with a shoulder at 450 nm, which disappears after reduction with lactose and corresponds to the absorption peak of the FAD cofactor. Kinetic characterisation with the cyt c assay and lactose as electron donor resulted in a neutral pH profile with an activity maximum at pH 5.5 and still 65% relative activity at pH 7.4 (**FIG 2.c**). The specific activity at pH 7.4 was 2.73 U/mg using the cyt c assay and glucose as substrate. The pH optimum of the flavin domain was obtained with the DCIP assay and shows a more acidic pH optimum, however, the flavin domain is sufficiently active at pH 7.4 also with this electron acceptor. Kinetic constants for glucose (obtained with the cyt *c* assay at pH 5.5) are a K_M of 260 mM and a k_{cat} of 8.8 s^{-1} for glucose, which shows in comparison to currently known enzymes a far better suitability of this enzyme for the proposed application.

[0093] To test the electrochemical behaviour of *Hypoxylon haematostroma* CDH on electrodes, the purified enzyme preparation was immobilised by adsorption on a spectroscopic graphite electrode surface. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the current at pH 7.4. The optimum pH under the chosen conditions is 7.5 and the maximum current was obtained at this pH and at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH (7.4) on the electrode surface for glucose was determined to be 49 mM and I_{max} = 55 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 383 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 2-20 mM.

Example 18: CDH of Neurospora crassa

[0094] A cellobiose dehydrogenase with high glucose turnover rates and activity under physiological pH conditions was obtained from liquid cultures of *Neurospora crassa.* The culture was grown and screened as described. The maximum activity under the chosen conditions was 156 U/L (cyt c assay, pH 6.0, 18th day).For enzyme production and purification the outlined procedures were applied and resulted in an CDH preparation with a specific activity of 10.6 U/mg (DCIP assay, pH 6.0), an apparent molecular weight of 90 kDa as determined by SDS-PAGE and an isoelectric point of 4.3. The calculated molecular weight of the obtained protein sequence is 86.283 kDa and fits well to the native CDH. The calculated isoelectric point is 6.68. The spectrum of Neurospora crassa CDH is typical and shows the haem alpha-, beta- and gamma-bands of the reduced enzyme at 563, 533 and 430 nm. In the oxidised enzyme the gamma-band has its absorption maximum at 421 nm with a shoulder at 450 nm, which disappears after reduction with lactose and corresponds to the absorption peak of the FAD cofactor. Kinetic characterisation with the cyt c assay and lactose as electron donor resulted in a neutral pH profile with an activity maximum at pH 6.0 and 52% relative activity at pH 7.4 (**FIG 2.d**). The specific activity at pH 7.4 was 1.04 U/mg using the cyt c assay and glucose as substrate. The pH optimum of the flavin domain was obtained with the DCIP assay and shows a more acidic pH optimum, however, the flavin domain is sufficiently active at pH 7.4 also with this electron acceptor. Kinetic constants for glucose (obtained with the cyt c assay at pH 5.5) are a K_M of 1680 mM and a kcat of 15.9 s^{-1} for glucose, which shows in comparison to other known enzymes a far better suitability of this enzyme for the proposed application.

[0095] To test the electrochemical behaviour of *Neurospora crassa* CDH on electrodes, the purified enzyme preparation was immobilised by adsorption on a spectroscopic graphite electrode surface. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the

current at pH 7.4. The optimum pH under the chosen conditions is 5.0 and 31% of the maximum current was obtained at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH on the electrode surface was determined to be 90 mM and I_{max} = 5 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 82 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 2-10 mM.

Example 19: CDH of *Stachybotris bisbyi*

[0096] A cellobiose dehydrogenase with high glucose turnover rates and activity under physiological pH conditions was obtained from liquid cultures of *Stachybotris bisbyi.* The culture was grown and screened as described. The maximum activity under the chosen conditions was 154 U/L (cyt c assay, pH 6.0, 24th day). For enzyme production and purification the outlined procedures were applied and resulted in a CDH preparation with a specific activity of 7.9 U/mg (DCIP assay, pH 6.0), an apparent molecular weight of 100 kDa as determined by SDS-PAGE and an isoelectric point of 4.5. The calculated molecular weight of the obtained protein sequence is 86.212 kDa and fits well to the native CDH when considering a glycosylation of 14% of *S. bisbyi* CDH, a value which lies within the observed range (2-15%, Zámocky et al., 2006, Current Protein and Peptide Science, 7: 255-280). The calculated isoelectric point is 6.37. The spectrum of *Stachybotris bisbyi* CDH is typical and shows the haem alpha-, beta- and gamma-bands of the reduced enzyme at 562, 533 and 430 nm. In the oxidised enzyme the gamma-band has its absorption maximum at 420 nm with a shoulder at 450 nm, which disappears after reduction with lactose and corresponds to the absorption peak of the FAD cofactor. Kinetic characterisation with the cyt c assay resulted in a pH profile with an activity maximum at pH 5.5 and 60% relative activity at pH 7.4 (**FIG 2.e**). The specific activity at pH 7.4 was 0.58 U/mg using the cyt c assay and glucose as substrate. The pH optimum of the flavin domain was obtained with the DCIP assay and shows a similar trend indicating that substrate oxidation by the enzyme is efficient at pH 7.4. Kinetic constants for glucose (obtained with the cyt c assay at pH 5.5) are a K_M of 950 mM and a k_{cat} of 14.1 s^{-1} for glucose, which shows in comparison to currently known enzymes a far better suitability of this enzyme for the proposed application.

[0097] To test the electrochemical behaviour of *Stachybotris bisbyi* CDH on electrodes, the purified enzyme preparation was immobilised by adsorption on a spectroscopic graphite electrode surface. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the current at pH 7.4. The optimum pH under the chosen conditions is 5.0 and 27% of the maximum current was obtained at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH on the electrode surface was determined to be 131 mM and I_{max} = 65 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 237 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 3-15 mM.

Example 20: CDH from *Myriococcum thermophilum*

[0098] CDH from *Myriococcum thermophilum* was found to oxidise glucose very efficiently (Harreither et al., 2007, Electroanalysis 19: 172-180), but not under physiological conditions. It was used as a protein scaffold for which DET at neutral pH was developed by means of genetic engineering. The enzyme variants D160K and D547S/E550S were obtained according to the described methods to increase the IET at pH 7.4 and thereby the electrode response in order to optimise the enzyme for applications under neutral or alkaline pH conditions.

[0099] For enzyme production and purification of the enzyme from the native producer, the protocol given in (Harreither et al., 2007, Electroanalysis 19: 172-180) was followed and resulted in a CDH preparation with a specific activity of 10.7 U/mg (DCIP assay, pH 6.0), an apparent molecular weight of 94 kDa and an isoelectric point of 3.8. The calculated molecular weight of the protein sequence is 86.701 kDa and fits well to the native CDH. The calculated isoelectric point is 4.62. The spectrum of CDH obtained from M. thermophilum is typical and shows the haem alpha-, beta- and gamma-bands of the reduced enzyme at 563, 533 and 429 nm. In the oxidised enzyme the gamma-band has its absorption maximum at 421 nm with a shoulder at 450 nm, which disappears after reduction with lactose and corresponds to the absorption peak of the FAD cofactor. Kinetic characterisation with the cyt c assay and lactose as electron donor resulted in a neutral pH profile with an activity maximum between pH 4.0-4.5 and 0% relative activity at pH 7.4 (**FIG 2.f**). The specific activity at pH 7.4 was also 0 U/mg using the cyt c assay and glucose as substrate. The pH optimum of the flavin domain was obtained with the DCIP assay and shows a far less acidic pH optimum (6.0), indicating that substrate oxidation at the flavin domain is performed even at neutral and slightly alkaline conditions efficiently, but the IET is rate limiting. The obtained kinetic constants for glucose (DCIP assay, pH 6.0; K_M = 250 mM, kcat = 14.2 s^{-1}) show that although glucose conversion is very efficient, M. thermophilum CDH is not suitable for the proposed application because no IET was measured above pH 7.0.

[0100] The recombinant enzyme variants were produced heterologeously in *P. pastoris* according to the explained routines. The molecular weights, isoelectric points or spectral properties did not differ significantly from the native enzyme produced by the fungus.

[0101] Kinetic characterisation of D160K with the cyt c assay and lactose as electron donor resulted in a pH with an activity maximum at 5.0 and 24% relative activity at pH 7.4 (**FIG 2.g**). The specific activity at pH 7.4 was 1.01 U/mg using the cyt c assay and glucose as substrate. To test the electrochemical behaviour of D160K on electrodes, the purified enzyme preparation was immobilised by adsorption on a screen printed electrode. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the current at pH 7.4. The optimum pH under the chosen conditions is 5.5 and 52% of the maximum current was obtained at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH on the electrode surface was determined to be 133 mM and I_{max} = 105 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 513 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 0.5-20 mM.

[0102] Kinetic characterisation of D547S/E550S with the cyt c assay and lactose as electron donor resulted in a pH with an activity maximum between 4.5 and 5.0 and 13% relative activity at pH 7.4 (**FIG 2.h**). The specific activity at pH 7.4 was 0.70 U/mg using the cyt c assay and glucose as substrate. To test the electrochemical behaviour of D547S/E550S on electrodes, the purified enzyme preparation was immobilised by adsorption on a graphite electrode surface. Using a flow cell and subsequent injections of 50 mM glucose, DET currents were determined to determine the pH optimum, the current at the pH optimum and the current at pH 7.4. The optimum pH under the chosen conditions is 5.5 and 24% of the maximum current was obtained at pH 7.4 in 10 mM phosphate buffered saline (PBS) containing 100 mM NaCl. The K_M value of the heterogenised enzyme at optimum pH on the electrode surface was determined to be 55 mM and I_{max} = 30 nA. The currents obtained in glucose measurements should therefore follow a nearly linear relationship for concentrations approx. five-fold below the K_M value. The DET current density obtained at pH 7.4 was 241 nA/cm^2 and the linear range for glucose detection at pH 7.4 with the chosen setup within 1-20 mM.

Example 21: Sequences

[0103]

>M.thermophilum (SEQ ID NO: 1)

mrtssrligalaaallpsalaqnnvpntftdpdsgitfntwgldedspqtqggftfgvalpsdalttdasefigylkcarndesgw
cgislggpmtnsllitawphedtvytslrfatgyampdvyegdaeitqvsssvnsthfslifrcknclqwshggssggastsggvl
vlgwvqafddpgnptcpeqitlqqhdngmgiwgaqlntdaaspsytdwaaqatktvtgdcegptetsvvgvpvptgvsfdyivvgg
gaggipaadklseagksvlliekgfastantggtlgpewleghdltrfdvpglcnqiwvdskgiacedtdqmagcvlgggtavnag
lwfkpysldwdylfpdgwkyndvqpainralsripgtdapstdgkryyqegfevlskglaaggwtsvtannapdkknrtfahapfm
faggerngplgtyfqtakkrnnfdvwlntsvkrviregghitgvevepfrdggyegivpvtkvtgrvilsagtfgsakillrsgig
pedqlevvaasekdgptmignsswinlpvgynlddhlntdtvishpdvvfydfyeawddpiesdknsylesrtgilaqaapnigpm
fweeivgadgivrqlqwtarvegslgapnghtmtmsqylgrgatsrgrmtitpslttivsdvpylkdpndkeaviqgiinlqnalq
nvanltwlfpnstitpreyvesmvvspsnrrsnhwmgtnklgtddgrkggsavvdldtrvygtdnlfvidasifpgvpttnptsyi
vvaaehassrilalpdlepvpkygqcggrewtgsfvcadgstceyqnewysqcl

>H.haematostroma (SEQ ID NO: 3)

mgrlgslaklllavglnvqqcfgqngpptpytdsetgitfatwsggnglapwggltfgvalpenalttdateligylkcgsngttt
dawcglsfggpmtnslllmawphedeiltsfrfasgytrpdlytgdakltqisstidkdhftlifrcqnclawnqdgasgsastsa
gslilgwasalraptnagcpaeinfnfhnngqmiwgatldesaanpsysewaakatatvtgdcggatpttttttttsvptatgipv
ptgtydyivvgagaggipladklseagksvlliekgppssgrwggtlkpewlkdtnltrfdvpglcnqiwvnsagvactdtdqmag
cvlgggtavnaglwwkpynldwdynfprgwksrdmaaatrrvfsripgtdnpsmdgkrylqqgfeilagglkaagwtevtandapn
kknhtyshspfmfsggerggpmgtylvsasrrknfhlwtgtavkrvvrtgghitglevepfvnggytgvvnvtsitgrvvlsagaf
gsakillrsgigpedqleivksstdgptmisdsswitlpvgynledhtntdtvvthpdvvfydfyeaghpnvtdkdlylnsragil
aqaapnigpmfweeikgrdgvvrqlqwtarvegsagtpngyamtmsqylgrgaksrgrmtitkalttvvstvpylqdkndveaviq
giknlqaalsnvknltwayppsnttvedfvnnmlvsytnrrsnhwigtnklgtddgrsrggsavvdlntkvygtdnlfvvdagifp
ghittnptsyiviaaeraserildlpparaqprfaqcggrtwtgsfqcaapytcqyrnerysqcr

>C.attrobruneum (SEQ ID NO: 5)

mrpssrfvgalaaaasflpsalaqnnaavtftdpdtgivfnswglangapqtqggftfgvalpsdalttdatefigylecasadnq
gwcgvsmggpmtnsllitawphednvytslrfatgyampdvysgdatitqisssinathfklifrcqnclqwthdgasggastsag
vlvlgwvqafpspgnptcpdqitleqhnngmgiwgavmdsnvanpsytewaaqatktveaecdgpsetdivgvpvptgttfdyivv

gggaggiptadklseagksvlliekgiastaehggtlgpewlegndltrfdvpglcnqiwvdskgiacedtdqmagcvlgggtavn
aglwfkpysldwdylfpsgwkyrdiqaaigrvfsripgtdapstdgkryyqqgfdvlagglsaggwnkvtansspdkknrtfsnap
fmfsggerggplatyltsakkrsnfnlwlntsvkrviregghvtgvevepfrtggyqgivnvtavsgrvvlsagtfgsakillrgg
igpadqlevvkaskidgptmisnaswiplpvgynlddhlntdtvithpdvafydfyeawntpieadknsylssrtgilaqaapnig
pmmweeikgadgivrqlqwtarvegsfdtpngqamtisqylgrgatsrgrmtitpslttvvsdvpylkdpndkeaviqgivnlqna
lknvagltwtypnssitpreyvdnmvvspsnrranhwmgtakigtddgrlaggsavvdlntkvygtdnlfvvdasifpgtpttnps
ayivtaaehasqrilglaapkpvgkwgqcggrqwtgsfqcvsgtkcevvnewysqcl

>C.thermophilum (SEQ ID NO: 7)

mkllsrvgatalaatlslkqcaaqmtegtytheatgitfktwtpsdgstftfglalpgdaltndateyigllrcqitdpsspgycg
ishgqsgqmtqalllvawasedvvytsfryatgytlpelytgdakltqiassvsgdsfevlfrcencfswdqngatgsvstsngal
vlgyaasksgltgatcpdtaefgfhnngfgqwgavlegatsdsyeewaqlatitppttcdgngpgdkvcvpapedtydyivvgaga
ggitvadklseaghkvlliekgpppstglwngtmkpewlegtdltrfdvpglcnqiwvdsagiactdtdqmagcvlgggtavnaglw
wkphpadwddnfphgwkssdladatervfsripgtwhpsqdgklyrqegfevisqglanagwrevdanqepseknrtyshsvfmfs
ggerggplatylasaaqrsnfnlwvntsvrrairtgprvsgvelecladggfngtvnlkegggvifsagafgsaklllrsgigped
qleivasskdgetfiskndwiklpvghnlidhlntdliithpdvvfydfyaawdnpitedkeaylnsrsgilaqaapnigplmwee
vtpsdgitrqfqwtcrvegdssktnsthamtlsqylgrgvvsrgrmgitsgltttvaehpylhndgdleaviqgiqnvvdalsqvp
dlewvlpppnttveeyvnslivspanrranhwmgtakmglddgrsggsavvdlntkvygtdnlfvvdasifpgmstgnpsamiviv
aeqaaqrilslry

>S.bisbyi (SEQ ID NO: 9)

mlfklsnwllalalfvgnvvaqlegptpytdpdtgivfqswvnpagtlkfgytypanaatvaatefigflecqgagwcsvslggsm
lnkplvvaypsgdevlaslkwatgyanpepyggnhklsqisssvtsagfrvvyrcegclawnyqgieggsptngasmpigwaysas
svlngdcvdntvliqhdtfgnygfvpdesslrteyndwtelptrvvrgdcggstttssvpsstappqgtgipvptgasydyivvgs
gaggipiadklteagkkvlliekgppssgrydgklkptwlegtnltrfdvpglcnqiwvdsagiacrdtdqmagcvlgggtavnag
lwwkpnpidwdynfpsgwkssemigatnrvfsriggttvpsqdgktyyqqgfnvlssglkaagwtsvslnnapaqrnrtygagpfm
fsggerggplatylatakkrgnfdlwtntqvkrvirqgghvtgvevenyngdgykgtvkvtpvsgrvvlsagtfgsaklllrsgig
pkdqlaivknstdgptmaserdwinlpvgynledhtntdivishpdvvhydfyeawtasiesdktaylgkrsgilaqaapnigplf
fdevrgadnivrsiqytarvegnsvvpngkamvisqylgrgavsrgrmtisqglntivstapylsnvndleaviksleniansltS
kvknlkiewpasgtsirdhvtnmpldpatrranhwigtnkigtkngrltggdsvvdlntkvygtdnlfvvdasifpgmvttnpsay
iviaaehaaskilslptakaaakyeqcggleyngnfqcasgltctwlndyywqct

>N.crassa (SEQ ID NO: 11)

MRTTSAFLSGLAAVASLLSPAFAQTAPKTFTHPDTGIVFNTWSASDSQTKGGFTVGMALPSNALTTDATE
FIGYLECSSAKNGANSGWCGVSLRGAMTNNLLITAWPSDGEVYTNLMFATGYAMPKNYAGDAKITQIASS
VNATHFTLVFRCQNCLSWDQDGVTGGISTSNKGAQLGWVQAFPSPGNPTCPTQITLSQHDNGMGQWGAAF
DSNIANPSYTAWAAKATKTVTGTCSGPVTTSIAATPVPTGVSFDYIVVGGGAGGIPVADKLSESGKSVLL
IEKGFASTGEHGGTLKPEWLNNTSLTRFDVPGLCNQIWKDSDGIACSDTDQMAGCVLGGGTAINAGLWYK
PYTKDWDYLFPSGWKGSDIAGATSRALSRIPGTTTPSQDGKRYLQQGFEVLANGLKASGWKEVDSLKDSE
QKNRTFSHTSYMYINGERGGPLATYLVSAKKRSNFKLWLNTAVKRVIREGGHITGVEVEAFRNGGYSGII

PVTNTTGRVVLSAGTFGSAKILLRSGIGPKDQLEVVKASADGPTMVSNSSWIDLPVGHNLVDHTNTDTVI
QHNNVTFYDFYKAWDNPNTTDMNLYLNGRSGIFAQAAPNIGPLFWEEITGADGIVRQLHWTARVEGSFET
PDGYAMTMSQYLGRGATSRGRMTLSPTLNTVVSDLPYLKDPNDKAAVVQGIVNLQKALANVKGLTWAYPS
ANQTAADFVDKQPVTYQSRRSNHWMGTNKMGTDDGRSGGTAVVDTNTRVYGTDNLYVVDASIFPGVPTTN
PTAYIVVAAEHAAAKILAQPANEAVPKWGWCGGPTYTGSQTCQAPYKCEKQNDWYWQCV

>M.thermophilum (SEQ ID NO: 2)

atgaggacctcctctcgtttaatcggagcccttgcggcggcacttttgccgtctgcccttgcccagaacaatgtcccgaatacttt
taccgaccctgactcgggcatcaccttcaacacgtggggtctcgacgaggattctccccagactcagggcggtttcaccttcggcg
ttgccctgccctctgatgccctcacaaccgacgcctcggaatttatcggttacttgaaatgcgcaaggaatgatgagagcggttgg
tgtggcatttcccttggcgggcctatgaccaactcgctcctcatcacagcctggccgcacgaggacacggtctacaccagtcttcg
gttcgcgaccggttacgccatgccggatgtctacgaggggacgccgagattacccaggtctcttcctctgttaattcgacgcact
tcagtctcatcttcaggtgcaagaactgcctgcaatggagccacggcggctcctccggcggcgcctctacctcgggcggcgtgttg
gtactcggctgggttcaggcattcgacgatcccggcaatccaacctgccccgagcagatcacactccagcagcacgacaacggcat
gggtatctggggtgcccagctcaacacggatgctgccagcccgtcctacactgactgggccgcccaggctaccaagaccgtcaccg
gtgactgcgagggccccaccgagacttctgtcgtcggcgtccccgttccgacgggtgtctcgttcgattatattgttgtcggcggc
ggcgccgggggcatccccgcagctgacaagctcagcgaggccggcaagagtgtgttgctcatcgagaagggctttgcttcgaccgc
aaacaccggaggtactctcggccctgaatggcttgagggccatgatctgacccgcttcgacgtgccgggtctgtgcaaccagatct
gggtcgattccaaggggatcgcttgcgaggataccgaccagatggctggctgtgttctcggcggcggcaccgccgtgaatgctggc
ctgtggttcaagccctactcgctcgactgggactacctcttccccgatggttggaagtacaatgacgtccagcctgccatcaaccg
cgccctctcgcgcatcccaggcaccgacgccccttctaccgacggaaagcgctactaccaggagggttttgaggtcctctccaagg
gcctggccgccggcggctggacctcagtcacggccaataatgcgcccgacaagaagaaccgcaccttcgcccatgctcccttcatg
tttgccggcggcgagcgcaatggccctctgggtacctacttccagactgccaagaagcgcaacaatttcgatgtctggctcaacac
gtcggtcaagcgcgtcatccgtgagggtggccacatcaccggcgtcgaggtcgagccgttccgtgacggtggttacgagggcattg
tccccgtcaccaaggttaccggccgcgttatcctgtctgccggcaccttcggcagtgcaaagattctgttaaggagcggtattggc
ccggaagatcagctagaagttgtcgcggcctccgagaaggacggccctaccatgatcggcaactcgtcctggatcaacctgcctgt
cgggtacaacctcgatgaccatctcaacaccgacacagtcatctcccaccccgatgtcgtgttctacgacttttacgaggcgtggg
atgatcccatcgagtctgacaagaatagctatctcgaatcgcgtacgggcatcctcgcccaagccgctcccaacattggccctatg
ttctgggaagagatcgtgggcgcggacggcatcgttcgccagctccagtggactgcccgtgtcgagggtagcctgggcgctcccaa
cggccacactatgaccatgtcgcagtaccttggccgtggtgccacctcacgcggccgcatgaccatcaccccgtctctgacgacta
tcgtctcagacgtgccttacctcaaagaccccaacgacaaggaggctgtcatccaaggcatcatcaacctgcagaacgcccttcag
aacgtcgccaacctgacttggctcttccccaactctaccattacgccgcgcgaatacgttgagagcatggtcgtctccccgagcaa
ccggcggtccaaccactggatgggcaccaacaagctcggtaccgacgacgggcggaagggtggctccgctgtcgtcgacctcgaca
ccagggtctacggtactgacaacctcttcgtcatcgacgcctccatcttccccggcgtgcccaccacgaatcctacttcgtacatc
gtggtagcggcagagcacgcttcgtcccgcatcctcgccctgcccgacctcgagcccgtccccaagtacggccagtgtggcggtcg
cgaatggaccggtagcttcgtctgcgccgatggttccacgtgcgagtaccagaatgagtggtactcgcagtgcttgtga

>H.haematostroma (SEQ ID NO: 4)

atgggtcgcctaggctctctcgcgaagttgcttctcgcagtcggcttgaatgttcagcaatgcttcgggcaaaacggacccccgac
cccctacactgatagtgagaccggtatcactttcgccacctggtccggcggaaacggcttagcaccctggggcggcttgactttcg

gtgttgcgttacctgaaaatgccctgaccaccgacgctaccgagctgattggatacctgaaatgcggttccaatggcacaaccaca
gatgcgtggtgtggtctgtcgtttgggggcccgatgactaacagcctccttctcatggcctggccgcacgaagacgagatcttgac
atcattccgttttgccagtggatataccagaccagacctatacaccggcgatgccaaattaacgcagatatcatccaccatcgata
aagatcactttactctaattttcaggtgccagaactgtctagcgtggaaccaagacggcgcgtctggttccgcttcaactagtgcc
ggctccttgatattaggctgggccagtgcgcttcgggccccgacgaatgcaggctgtccggctgaaatcaacttcaacttccacaa
caatggccagatgatatggggcgctacattagacgagagcgccgcaaacccatcatattcggaatgggctgccaaagccaccgcta
cggttaccggtgactgcggcggtgcaacccctacgaccactactaccaccaccacgtccgtccctaccgccacaggtatcccagtg
ccaactggcacctacgactatattgtagttggtgcgggtgctggcggaatacctttggccgacaagctgagcgaggctggaaagag
tgtgttactgatcgaaaaggggccgccatcatcgggacgatggggtggcaccctcaagccagagtggttgaaggacaccaacttga
cacggtttgacgtccctggcctgtgcaatcagatctgggtcaactctgcaggcgtcgcttgtactgacacagaccaaatggccggt
tgcgttcttggtggtggtacagctgtcaacgctggcctatggtggaagccctacaacctcgactgggattataacttcccacgcgg
atggaagtccagggatatggccgctgcaaccaggagagtcttctctcgcattcccggtacagataatccctcaatggatggcaagc
ggtatttacagcaaggcttcgaaatcctcgctggtggcttgaaagccgctggatggaccgaggttaccgcgaatgacgcacccaat
aagaagaaccacacctactcacactcgccgttcatgttctccggcggcgaacggggtggcccaatgggcacctacctggtatcggc
cagtagacgtaagaatttccatctatggacgggaacagcagtgaagagggttgttcgcacaggcggccatatcaccggtctggagg
tcgagcccttcgtaaacggcggttataccggtgttgtcaacgtcacctcgattactggtcgggtcgtcttgtctgctggtgcgttc
gggtcggctaagatattactgaggagcggcatcggacctgaggatcagttggagattgtcaagtcatcaaccgatggcccgaccat
gatttccgattcttcttggattacgctacccgtcggttataatctagaggatcacacaaacaccgacacggtcgttacgcatcctg
acgtcgtattttacgacttctacgaggctggacatcctaatgttaccgacaaggacttgtatctcaactcacgggccggaatcctt
gctcaagcagcgcctaatatcggcccaatgttctgggaagagattaagggtagggacggcgtcgttagacagctccagtggacagc
cagagttgaaggaagtgccggtacaccgaatgggtacgccatgacaatgagccaatacctttggacgaggcgctaagtcgaggggcc
gaatgactatcacgaaggcgttgacgaccgtcgtttctacagtaccttacctacaggataagaacgacgtggaagcagtcatccag
ggaatcaagaaccttcaagcagcactttcgaacgtgaagaatctcacatgggcctacccaccatctaatacgacggtggaggactt
tgttaacaacatgctggtttcatacactaataggcgttccaaccactggattgggaccaacaagctcggaaccgatgatggccgat
cgcgcggaggttcagctgtcgtggacctcaacactaaggtatacggcaccgacaacctgttcgtcgttgacgcaggaatattcccc
ggtcatattaccacgaacccgacttcgtatatcgtgatcgccgctgagcgcgcttctgagaggatcctcgaccttcccccggctag
agcacaaccgcgcttcgcgcagtgcggcgggcgaacgtggacgggtagcttccagtgtgcagcgccgtacacttgtcagtacagga
atgagcggtattcccagtgccggtaa

>C.attrobruneum (SEQ ID NO: 6)

atgaggccctcctctcggtttgttggtgccctggcggcggcggcgtcgttcctgccgtctgcccttgcccagaacaatgctgcagt
cacctttcactgacccggacaccggcatcgtcttcaactcctggggtcttgccaatggagcaccacagactcagggaggcttcacct
ttggtgtcgctctgccctctgatgcgctcacgaccgatgctaccgagttcattggttatttggaatgtgcctccgcggacaaccag
ggctggtgcggtgtctcgatgggcggccccatgaccaactcgcttcttatcaccgcctggccgcacgaggacaacgtctacacctc
cctccggtttgcaacaggatacgccatgccggatgtctactcgggagacgccaccatcacgcagatctcgtcgagcatcaacgcga
cccacttcaagctcatcttcaggtgccagaactgcctgcaatggacccacgacggcgcttccggtggcgcctccacgtctgccggt
gttctggtcctcggctgggtccaggctttcccttcccctggcaacccgacgtgcccggaccagatcacgctcgagcagcacaacaa
cggcatgggcatctggggtgcggtgatggactccaacgtcgccaacccgtcctacacagagtgggccgcgcaggccaccaagacgg
tcgaggccgagtgcgacggcccgagtgagacggatattgtcggcgtgcccgtgccgaccggcaccaccttcgactacatcgtcgtg
ggcggcggtgccggcggtatccccactgccgacaagctcagcgaggccggcaagagtgtgctgctgattgagaagggcatcgcctc

gactgctgagcacggcggcactctcggacccgagtggctcgagggcaacgacctgacgcggttcgacgtgcccggtctttgcaacc
agatctgggttgactccaagggcatcgcctgcgaggacaccgaccagatggccggttgcgtcctcggcggcggcacggccgtcaac
gccggcctctggttcaagccctactcgctcgactgggactacctcttcccaagcggctggaagtaccgcgacatccaggccgccat
cggcagggtgttctcgcgcatcccgggcactgacgcgccctcgaccgacggcaagcgctactaccagcagggcttcgacgtgctcg
cgggcggcctgagtgccggcggctggaacaaggtcacggccaactcgtctccagacaagaagaaccgcaccttctcgaacgcgcct
ttcatgttctcgggcggcgagcgcggcgggcccctggccacttatctcaccagcgccaagaagcgcagcaacttcaacctgtggct
caacacgtcggtcaagcgcgtcatccgtgagggcggccacgtcacaggtgtcgaggtcgagcctttccggacgggcgggtaccagg
gtatcgtgaacgttaccgccgtttcgggccgtgtcgtcctgtcggctggtaccttcggcagtgccaagattctgctcagaggcggt
attggcccagcggatcagctcgaggttgtcaaggcgtcgaagatcgacgggccgaccatgatcagcaatgcgtcttggattcctct
gcctgttgggtacaacctggatgaccatctcaacactgacactgtcattacccaccccgacgttgccttctacgacttctacgagg
catggaacacgcccattgaggcggacaagaacagctacctgagcagccgcactggtatcctcgctcaggccgcgcccaacattggc
ccaatgatgtgggaggaaatcaagggtgccgacggtatcgtccgccagctgcaatggaccgcccgtgtcgagggtagctttgacac
gcctaacgggcaggcgatgaccatctcgcagtacctcggccgcggcgcgacctcgcgcggccgtatgaccatcacccttcgctga
cgaccgtcgtctcggacgtgccgtacctcaaggacccgaacgataaggaggccgtcatccagggcatcgtcaacctgcagaacgcc
ctcaaaaacgtcgccggcctgacctggacctaccccaactcgagcatcacaccgcgcgaatacgtcgataatatggtagtctcccc
tagcaaccggcgcgcaaaccactggatgggcacggccaaaatcggcaccgacgacggccgcctggccggcggctccgccgtcgtgg
acttgaacaccaaggtctacggcaccgacaacctctttgtcgtggacgcgtccatcttccccggcacgcccaccaccaatccctcg
gcgtacatcgtcacggctgcggagcatgcttcgcagaggatcttggggttggctgcgccgaagccggttgggaaatggggccagtg
tggcgggcggcagtggacagggagcttccagtgcgtgagtgggacaaagtgtgaggtggtgaatgagtggtactcgcagtgcttgt
ag

>C.thermophilum (SEQ ID NO: 8)

atgaagcttctcagccgcgttggggccaccgccctagcggcgacgttgtccctgaaacaatgtgcagctcagatgaccgaagggac
gtacacccatgaggctaccggtatcacgttcaagacatggactccttccgacggctcgactttcactttcggcttggccctccctg
gggacgcgctgacaaatgatgccaccgagtacattggtctcctgcgttgccaaatcaccgatccctcttcgcccggctactgtggc
atctcccacggccagtccggccagatgacgcaggcgctgctgctggtcgcttgggccagcgaggatgtcgtctacacgtcgttccg
ctacgccaccggctacacactccccgagctctacacgggcgacgccaagctgacccagatcgcctcctcggtcagcggggacagct
tcgaggtgctgttccgctgcgagaactgcttctcctgggaccagaacggcgccacgggcagtgtctcgaccagcaacggcgccctg
gttctcggctacgctgcctcgaagagtggtttgacgggcgccacgtgcccggacacggccgagtttggcttccacaacaatggttt
cggacagtggggtgcagtgctcgagggtgcgacctcggactcgtatgaggagtgggctcagctggccactatcacgccccgacca
cctgcgatggcaacggccctggcgacaaggtgtgcgttccggctcccgaagacacgtatgattacatcgttgtcggcgccggcgcc
ggcggcatcacggtcgccgacaagctcagcgaggccggccacaaggtcctccttatcgagaagggtcctccgtcgaccggcctgtg
gaacgggaccatgaagcccgagtggctcgagggtaccgacctcacccgcttcgacgtccccggtctgtgcaaccagatctgggtcg
actctgccggcattgcctgcaccgataccgaccagatggcgggctgcgttctcggcggtggcaccgctgtcaatgctggtctgtgg
tggaagccccaccccgctgactgggacgacaacttccctcatggctggaagtcgagcgatctcgcggatgcgaccgagcgtgtctt
cagccgcattcccggcacgtggcacccgtcgcaggatggcaaactgtaccgccaggagggcttcgaggtcatcagccagggcctgg
ccaacgccggctggagggaagtcgacgccaaccaggagcccagcgagaagaaccgcacgtattcccacagtgtgttcatgttctcg
ggcggtgagcgcggcggcccccctggcgacgtacctcgcctcggctgcccagcgcagcaacttcaacttgtgggtcaacacttcggt
ccggagggccatccgcaccggccccagggtcagtggcgtcgaactcgagtgccttgcggacggcggcttcaacggtactgtcaacc
tgaaggagggtggtggtgtcatcttttcggctggcgctttcggctcggccaagctgctccttcgcagcggcatcggtcctgaggac

cagctcgagattgtggcgagctccaaggacggcgagaccttcatttccaagaatgattggatcaagctccccgtcggccataacct
gatcgatcatctcaacaccgacctcattattactcacccggatgtcgttttctatgacttctacgcggcttgggacaatcccatca
ccgaggacaaggaggcctacctgaactcgcggtccggcattctcgcccaagcggcgcccaacatcggccctctgatgtgggaggaa
gtcacgccatccgacggcatcacccgccagttccagtggacatgccgtgttgagggcgacagctccaagaccaactcgacccacgc
catgaccctcagccagtatctcggccgtggcgtcgtctcgcgcggccggatgggcatcacttccgggctgaccacgacggtggccg
agcacccgtacctgcacaacgacggcgacctggaggcggtgatccagggtatccagaacgtggtggacgcgctcagccaggtgccc
gacctcgagtgggtgctcccgccgcccaacacgacggtggaggaatacgtcaacagcctgatcgtgtctccggctaaccgccgggc
caaccactggatgggcacggccaagatgggcctcgatgacggccgctcgggcggctccgcggtcgtcgacctcaacacaaaggtgt
atggcaccgacaacctgtttgtcgtcgacgcctccatcttccctggcatgtcgacgggcaacccgtcggctatgatcgtcatcgtg
gccgagcaggcggcccagcgcatcctgtccctgcggtattag

>S.bisbyi (SEQ ID NO: 10)

atgctgttcaagctctcaaattggttgctagcgcttgcgctctttgttggcaatgtcgttgctcaactcgaggggcctaccccgta
cacggatccagataccggcattgtctttcagtcctgggtcaatccagcagggaccctgaagtttggttacacttaccccgcaaatg
ctgctacggttgccgccacggaatttatcggtttcctggaatgccaaggggctggatggtgtagcgtctcactcggtggctccatg
cttaacaagccgcttgttgttgcctaccctagtggcgatgaagtcctcgcttctttgaagtgggccacaggctacgcgaatccaga
gccttacggcggcaatcacaagctgtcccagatcagctcgtccgtcacctctgctggcttcagggtcgtctatcgatgtgagggat
gtctcgcctggaactaccagggaattgagggagggagccccaccaatggtgcgtccatgcctatcggttgggcttacagcgcaagt
tctgtactcaacggggattgtgtggataacactgttctcattcaacatgacacctttggcaattatggcttcgtacctgatgaatc
atctcttcgcacggagtacaatgactggacggagcttccgaccagggttgtcaggggagactgcggcggttccacaactacctctt
cggtgccctcctcaacggcgcctcctcaaggtactggcataccggttcctactggcgcaagctatgactacatagttgttggctcg
ggtgctggaggtattcccattgcggataagcttaccgaggctggcaaaaaggttttgttgattgagaagggaccaccctcttctgg
tcgctacgatggaaagctaaagccgacgtggcttgagggaactaatctcacccgattcgatgtgcctggcctctgcaaccaaatat
gggtcgactccgctggcattgcatgccgtgataccgatcagatggctggttgtgttcttggcggtggtactgctgtcaatgcaggt
ctatggtggaagcctaaccctattgatgggactataatttcccttcaggctggaagtcaagcgagatgataggcgcgacaaaccg
tgtcttttcacgtattggtggtactactgttccttcgcaggacggaaagacctactatcagcaaggtttcaacgttctttccagcg
gtctcaaggctgcgggctggacatctgttagcctgaataacgcccctgcgcaaaggaaccgcacctatggtgctggccctttcatg
ttctctggtggagagcgaggtggacctttggccacctacctggccactgccaagaagagaggaaacttcgacctctggacgaatac
ccaagttaagcgtgtaattcgacagggaggtcatgttactggagtggaggtcgaaaactataacggtgatgggtacaagggcactg
tcaaggtgactcctgtatctgggcgagttgtcctatctgctggtacctttggcagtgctaagcttttgctccgaagcggtatcggt
cccaaggatcaactagctattgtcaagaactcgactgatggccctactatggcttccgagagggactggattaatcttcccgttgg
ctacaacttggaggaccatactaacaccgacattgtcatctcccatccagatgtggtccattacgacttctatgaggcttggacag
cgtcaatcgagtctgacaagactgcttatttgggcaagcgttctggcatcctcgctcaagccgcccccaacatcgggcctctcttc
tttgacgaagttcgcggtgctgacaacattgtccgctcaattcagtacactgctcgtgtggagggcaacagtgtggtccctaatgg
caaggccatggtgatcagccagtaccttggtcgtggcgctgtttccaggggtcgaatgaccatctctcaaggtctcaatacgattg
tttccaccgctccatacctctcaaacgtcaatgatctcgaggccgtcattaagagccttgagaacatagcgaacagcttgacgtca
aaggttaaaaacctcaagattgaatggcctgcctctggtacatccattcgcgatcacgtcacgaatatgcctctcgacccggccac
ccgccgagcgaatcattggattggcactaacaagatcggaaccaagaatggtcgactgacaggtggtgattccgtcgttgatttga
acactaaggtctatggtacagacaatctgtttgtggtcgatgcttctattttccctggcatggttacgaccaacccctcggcctac
attgtaattgccgctgagcatgctgcatcgaagattctgagcctacctactgctaaggctgccgcgaagtacgaacaatgtggtgg

ccttgaatataatggtaactttcagtgtgcgtctggattaacctgcacttggttaaacgactactactggcagtgtacttaa

>N.crassa (SEQ ID NO: 12)

atgaggaccacctcggcctttctcagcggcctggcggcggtggcttcattgctgtcgcccgccttcgcccaaaccgctcccaagac
cttcactcatcctgataccggcattgtcttcaacacatggagtgcttccgattcccagaccaaaggtggcttcactgttggtatgg
ctctgccgtcaaatgctcttactaccgacgcgactgaattcatcggttatctggaatgctcctccgccaagaatggtgccaatagc
ggttggtgcggtgtttctctcagaggcgccatgaccaacaatctactcattaccgcctggccttctgacggagaagtctacaccaa
tctcatgttcgccacgggttacgccatgcccaagaactacgctggtgacgccaagatcacccagatcgcgtccagcgtgaacgcta
cccacttcacccttgtctttaggtgccagaactgtttgtcatgggaccaagacggtgtcaccggcggcatttctaccagcaataag
ggggcccagctcggttgggtccaggcgttcccctctcccggcaacccgacttgccctacccagatcactctcagtcagcatgacaa
cggtatgggccagtggggagctgcctttgacagcaacattgccaatccctcttatactgcatgggctgccaaggccaccaagaccg
ttaccggtacttgcagtggtccagtcacgaccagtattgccgccactcctgttcccactggcgtttcttttgactacattgtcgtt
ggtggtggtgccggtggtattcccgtcgctgacaagctcagcgagtccggtaagagcgtgctgctcatcgagaagggtttcgcttc
cactggtgagcatggtggtactctgaagcccgagtggctgaataatacatcccttactcgcttcgatgttcccggtctttgcaacc
agatctggaaagactcggatggcattgcctgctccgataccgatcagatggccggctgcgtgctcggcggtggtaccgccatcaac
gccggtctctggtacaagccctacaccaaggactgggactacctcttcccctctggctggaagggcagcgatatcgccggtgctac
cagcagagccctctcccgcattccgggtaccaccactccttctcaggatggaaagcgctaccttcagcagggtttcgaggttcttg
ccaacggcctcaaggcgagcggctggaaggaggtcgattccctcaaggacagcgagcagaagaaccgcactttctcccacacctca
tacatgtacatcaatggcgagcgtggcggtcctctagcgacttacctcgtcagcgccaagaagcgcagcaacttcaagctgtggct
caacaccgctgtcaagcgcgtcatccgtgagggcggccacattaccggtgtggaggttgaggccttccgcaacggcggctactccg
gaatcatccccgtcaccaacaccaccggccgcgtcgttctttccgccggcaccttcggcagcgccaagatccttctccgttccggc
attggccccaaggaccagctcgaggtggtcaaggcctccgccgacggccctaccatggtcagcaactcgtcctggattgacctccc
cgtcggccacaacctggttgaccacaccaacaccgacaccgtcatccagcacaacaacgtgaccttctacgacttttacaaggctt
gggacaaccccaacacgaccgacatgaacctgtacctcaatgggcgctccggcatcttcgcccaggccgcgcccaacattggcccc
ttgttctgggaggagatcacgggcgccgacggcatcgtccgtcagctgcactggaccgcccgcgtcgagggcagcttcgagacccc
cgacggctacgccatgaccatgagccagtaccttggccgtggcgccacctcgcgcggccgcatgaccctcagccctaccctcaaca
ccgtcgtgtctgacctcccgtacctcaaggaccccaacgacaaggccgctgtcgttcagggtatcgtcaacctccagaaggctctc
gccaacgtcaagggtctcacctgggcttaccctagcgccaaccagacggctgctgattttgttgacaagcaacccgtaacctacca
atcccgccgctccaaccactggatgggcaccaacaagatgggcaccgacgacggccgcagcggcggcaccgcagtcgtcgacacca
acacgcgcgtctatggcaccgacaacctgtacgtggtggacgcctcgattttccccggtgtgccgaccaccaaccctaccgcctac
attgtcgtcgccgctgagcatgccgcggccaaaatcctggcgcaacccgccaacgaggccgttcccaagtggggctggtgcggcgg
gccgacgtatactggcagccagacgtgccaggcgccatataagtgcgagaagcagaatgattggtattggcagtgtgtgtag

SEQUENCE LISTING

<110> Universität für Bodenkultur Wien

<120> Cellobiose Dehydrogenase

<130> r52433

<160> 32

<170> PatentIn version 3.5

<210> 1
<211> 828
<212> PRT
<213> Myriococcum thermophilum

<400> 1

```
Met Arg Thr Ser Ser Arg Leu Ile Gly Ala Leu Ala Ala Ala Leu Leu
1               5                  10                  15

Pro Ser Ala Leu Ala Gln Asn Asn Val Pro Asn Thr Phe Thr Asp Pro
            20                  25                  30

Asp Ser Gly Ile Thr Phe Asn Thr Trp Gly Leu Asp Glu Asp Ser Pro
        35                  40                  45

Gln Thr Gln Gly Gly Phe Thr Phe Gly Val Ala Leu Pro Ser Asp Ala
    50                  55                  60

Leu Thr Thr Asp Ala Ser Glu Phe Ile Gly Tyr Leu Lys Cys Ala Arg
65                  70                  75                  80

Asn Asp Glu Ser Gly Trp Cys Gly Ile Ser Leu Gly Gly Pro Met Thr
                85                  90                  95

Asn Ser Leu Leu Ile Thr Ala Trp Pro His Glu Asp Thr Val Tyr Thr
            100                 105                 110

Ser Leu Arg Phe Ala Thr Gly Tyr Ala Met Pro Asp Val Tyr Glu Gly
        115                 120                 125

Asp Ala Glu Ile Thr Gln Val Ser Ser Ser Val Asn Ser Thr His Phe
    130                 135                 140

Ser Leu Ile Phe Arg Cys Lys Asn Cys Leu Gln Trp Ser His Gly Gly
145                 150                 155                 160

Ser Ser Gly Gly Ala Ser Thr Ser Gly Gly Val Leu Val Leu Gly Trp
                165                 170                 175

Val Gln Ala Phe Asp Asp Pro Gly Asn Pro Thr Cys Pro Glu Gln Ile
            180                 185                 190

Thr Leu Gln Gln His Asp Asn Gly Met Gly Ile Trp Gly Ala Gln Leu
        195                 200                 205
```

```
Asn Thr Asp Ala Ala Ser Pro Ser Tyr Thr Asp Trp Ala Ala Gln Ala
210                 215                 220

Thr Lys Thr Val Thr Gly Asp Cys Glu Gly Pro Thr Glu Thr Ser Val
225                 230                 235                 240

Val Gly Val Pro Val Pro Thr Gly Val Ser Phe Asp Tyr Ile Val Val
                245                 250                 255

Gly Gly Gly Ala Gly Gly Ile Pro Ala Ala Asp Lys Leu Ser Glu Ala
            260                 265                 270

Gly Lys Ser Val Leu Leu Ile Glu Lys Gly Phe Ala Ser Thr Ala Asn
        275                 280                 285

Thr Gly Gly Thr Leu Gly Pro Glu Trp Leu Glu Gly His Asp Leu Thr
290                 295                 300

Arg Phe Asp Val Pro Gly Leu Cys Asn Gln Ile Trp Val Asp Ser Lys
305                 310                 315                 320

Gly Ile Ala Cys Glu Asp Thr Asp Gln Met Ala Gly Cys Val Leu Gly
                325                 330                 335

Gly Gly Thr Ala Val Asn Ala Gly Leu Trp Phe Lys Pro Tyr Ser Leu
            340                 345                 350

Asp Trp Asp Tyr Leu Phe Pro Asp Gly Trp Lys Tyr Asn Asp Val Gln
        355                 360                 365

Pro Ala Ile Asn Arg Ala Leu Ser Arg Ile Pro Gly Thr Asp Ala Pro
370                 375                 380

Ser Thr Asp Gly Lys Arg Tyr Tyr Gln Glu Gly Phe Glu Val Leu Ser
385                 390                 395                 400

Lys Gly Leu Ala Ala Gly Gly Trp Thr Ser Val Thr Ala Asn Asn Ala
                405                 410                 415

Pro Asp Lys Lys Asn Arg Thr Phe Ala His Ala Pro Phe Met Phe Ala
            420                 425                 430

Gly Gly Glu Arg Asn Gly Pro Leu Gly Thr Tyr Phe Gln Thr Ala Lys
        435                 440                 445

Lys Arg Asn Asn Phe Asp Val Trp Leu Asn Thr Ser Val Lys Arg Val
450                 455                 460

Ile Arg Glu Gly Gly His Ile Thr Gly Val Glu Val Glu Pro Phe Arg
465                 470                 475                 480

Asp Gly Gly Tyr Glu Gly Ile Val Pro Val Thr Lys Val Thr Gly Arg
```

485 490 495

Val Ile Leu Ser Ala Gly Thr Phe Gly Ser Ala Lys Ile Leu Leu Arg
500 505 510

Ser Gly Ile Gly Pro Glu Asp Gln Leu Glu Val Val Ala Ala Ser Glu
515 520 525

Lys Asp Gly Pro Thr Met Ile Gly Asn Ser Ser Trp Ile Asn Leu Pro
530 535 540

Val Gly Tyr Asn Leu Asp Asp His Leu Asn Thr Asp Thr Val Ile Ser
545 550 555 560

His Pro Asp Val Val Phe Tyr Asp Phe Tyr Glu Ala Trp Asp Asp Pro
565 570 575

Ile Glu Ser Asp Lys Asn Ser Tyr Leu Glu Ser Arg Thr Gly Ile Leu
580 585 590

Ala Gln Ala Ala Pro Asn Ile Gly Pro Met Phe Trp Glu Glu Ile Val
595 600 605

Gly Ala Asp Gly Ile Val Arg Gln Leu Gln Trp Thr Ala Arg Val Glu
610 615 620

Gly Ser Leu Gly Ala Pro Asn Gly His Thr Met Thr Met Ser Gln Tyr
625 630 635 640

Leu Gly Arg Gly Ala Thr Ser Arg Gly Arg Met Thr Ile Thr Pro Ser
645 650 655

Leu Thr Thr Ile Val Ser Asp Val Pro Tyr Leu Lys Asp Pro Asn Asp
660 665 670

Lys Glu Ala Val Ile Gln Gly Ile Ile Asn Leu Gln Asn Ala Leu Gln
675 680 685

Asn Val Ala Asn Leu Thr Trp Leu Phe Pro Asn Ser Thr Ile Thr Pro
690 695 700

Arg Glu Tyr Val Glu Ser Met Val Val Ser Pro Ser Asn Arg Arg Ser
705 710 715 720

Asn His Trp Met Gly Thr Asn Lys Leu Gly Thr Asp Asp Gly Arg Lys
725 730 735

Gly Gly Ser Ala Val Val Asp Leu Asp Thr Arg Val Tyr Gly Thr Asp
740 745 750

Asn Leu Phe Val Ile Asp Ala Ser Ile Phe Pro Gly Val Pro Thr Thr
755 760 765

Asn Pro Thr Ser Tyr Ile Val Val Ala Ala Glu His Ala Ser Ser Arg
770 775 780

Ile Leu Ala Leu Pro Asp Leu Glu Pro Val Pro Lys Tyr Gly Gln Cys
785 790 795 800

Gly Gly Arg Glu Trp Thr Gly Ser Phe Val Cys Ala Asp Gly Ser Thr
805 810 815

Cys Glu Tyr Gln Asn Glu Trp Tyr Ser Gln Cys Leu
820 825

<210> 2
<211> 2487
<212> DNA
<213> Myriococcum thermophilum

<400> 2
atgaggacct cctctcgttt aatcggagcc cttgcggcgg cacttttgcc gtctgccctt 60
gcccagaaca atgtcccgaa tacttttacc gaccctgact cgggcatcac cttcaacacg 120
tggggtctcg acgaggattc tccccagact cagggcggtt tcaccttcgg cgttgccctg 180
ccctctgatg ccctcacaac cgacgcctcg gaatttatcg gttacttgaa atgcgcaagg 240
aatgatgaga gcggttggtg tggcatttcc cttggcgggc ctatgaccaa ctcgctcctc 300
atcacagcct ggccgcacga ggacacggtc tacaccagtc ttcggttcgc gaccggttac 360
gccatgccgg atgtctacga gggggacgcc gagattaccc aggtctcttc ctctgttaat 420
tcgacgcact tcagtctcat cttcaggtgc aagaactgcc tgcaatggag ccacggcggc 480
tcctccggcg gcgcctctac ctcgggcggc gtgttggtac tcggctgggt tcaggcattc 540
gacgatcccg gcaatccaac ctgccccgag cagatcacac tccagcagca cgacaacggc 600
atgggtatct ggggtgccca gctcaacacg gatgctgcca gcccgtccta cactgactgg 660
gccgcccagg ctaccaagac cgtcaccggt gactgcgagg gccccaccga gacttctgtc 720
gtcggcgtcc ccgttccgac gggtgtctcg ttcgattata ttgttgtcgg cggcggcgcc 780
gggggcatcc ccgcagctga caagctcagc gaggccggca agagtgtgtt gctcatcgag 840
aagggctttg cttcgaccgc aaacaccgga ggtactctcg gccctgaatg gcttgagggc 900
catgatctga cccgcttcga cgtgccgggt ctgtgcaacc agatctgggt cgattccaag 960
gggatcgctt gcgaggatac cgaccagatg gctggctgtg ttctcggcgg cggcaccgcc 1020
gtgaatgctg gcctgtggtt caagccctac tcgctcgact gggactacct cttccccgat 1080
ggttggaagt acaatgacgt ccagcctgcc atcaaccgcg ccctctcgcg catcccaggc 1140
accgacgccc cttctaccga cggaaagcgc tactaccagg agggttttga ggtcctctcc 1200
aagggcctgg ccgccggcgg ctggacctca gtcacggcca ataatgcgcc cgacaagaag 1260
aaccgcacct tcgcccatgc tcccttcatg tttgccggcg gcgagcgcaa tggccctctg 1320
ggtacctact tccagactgc caagaagcgc aacaatttcg atgtctggct caacacgtcg 1380
gtcaagcgcg tcatccgtga gggtggccac atcaccggcg tcgaggtcga gccgttccgt 1440

gacggtggtt acgagggcat tgtccccgtc accaaggtta ccggccgcgt tatcctgtct 1500

gccggcacct tcggcagtgc aaagattctg ttaaggagcg gtattggccc ggaagatcag 1560

ctagaagttg tcgcggcctc cgagaaggac ggccctacca tgatcggcaa ctcgtcctgg 1620

atcaacctgc ctgtcgggta caacctcgat gaccatctca acaccgacac agtcatctcc 1680

caccccgatg tcgtgttcta cgacttttac gaggcgtggg atgatcccat cgagtctgac 1740

aagaatagct atctcgaatc gcgtacgggc atcctcgccc aagccgctcc caacattggc 1800

cctatgttct gggaagagat cgtgggcgcg gacggcatcg ttcgccagct ccagtggact 1860

gcccgtgtcg agggtagcct gggcgctccc aacggccaca ctatgaccat gtcgcagtac 1920

cttggccgtg gtgccacctc acgcggccgc atgaccatca ccccgtctct gacgactatc 1980

gtctcagacg tgccttacct caaagacccc aacgacaagg aggctgtcat ccaaggcatc 2040

atcaacctgc agaacgccct tcagaacgtc gccaacctga cttggctctt ccccaactct 2100

accattacgc cgcgcgaata cgttgagagc atggtcgtct ccccgagcaa ccggcggtcc 2160

aaccactgga tgggcaccaa caagctcggt accgacgacg ggcggaaggg tggctccgct 2220

gtcgtcgacc tcgacaccag ggtctacggt actgacaacc tcttcgtcat cgacgcctcc 2280

atcttccccg gcgtgcccac cacgaatcct acttcgtaca tcgtggtagc ggcagagcac 2340

gcttcgtccc gcatcctcgc cctgcccgac ctcgagcccg tccccaagta cggccagtgt 2400

ggcggtcgcg aatggaccgg tagcttcgtc tgcgccgatg gttccacgtg cgagtaccag 2460

aatgagtggt actcgcagtg cttgtga 2487

<210> 3
<211> 839
<212> PRT
<213> H. haematostroma

<400> 3

Met Gly Arg Leu Gly Ser Leu Ala Lys Leu Leu Leu Ala Val Gly Leu
1 5 10 15

Asn Val Gln Gln Cys Phe Gly Gln Asn Gly Pro Pro Thr Pro Tyr Thr
20 25 30

Asp Ser Glu Thr Gly Ile Thr Phe Ala Thr Trp Ser Gly Gly Asn Gly
35 40 45

Leu Ala Pro Trp Gly Gly Leu Thr Phe Gly Val Ala Leu Pro Glu Asn
50 55 60

Ala Leu Thr Thr Asp Ala Thr Glu Leu Ile Gly Tyr Leu Lys Cys Gly
65 70 75 80

Ser Asn Gly Thr Thr Thr Asp Ala Trp Cys Gly Leu Ser Phe Gly Gly
85 90 95

Pro Met Thr Asn Ser Leu Leu Leu Met Ala Trp Pro His Glu Asp Glu

100 105 110

Ile Leu Thr Ser Phe Arg Phe Ala Ser Gly Tyr Thr Arg Pro Asp Leu
115 120 125

Tyr Thr Gly Asp Ala Lys Leu Thr Gln Ile Ser Ser Thr Ile Asp Lys
130 135 140

Asp His Phe Thr Leu Ile Phe Arg Cys Gln Asn Cys Leu Ala Trp Asn
145 150 155 160

Gln Asp Gly Ala Ser Gly Ser Ala Ser Thr Ser Ala Gly Ser Leu Ile
165 170 175

Leu Gly Trp Ala Ser Ala Leu Arg Ala Pro Thr Asn Ala Gly Cys Pro
180 185 190

Ala Glu Ile Asn Phe Asn Phe His Asn Asn Gly Gln Met Ile Trp Gly
195 200 205

Ala Thr Leu Asp Glu Ser Ala Ala Asn Pro Ser Tyr Ser Glu Trp Ala
210 215 220

Ala Lys Ala Thr Ala Thr Val Thr Gly Asp Cys Gly Gly Ala Thr Pro
225 230 235 240

Thr Thr Thr Thr Thr Thr Thr Thr Ser Val Pro Thr Ala Thr Gly Ile
245 250 255

Pro Val Pro Thr Gly Thr Tyr Asp Tyr Ile Val Val Gly Ala Gly Ala
260 265 270

Gly Gly Ile Pro Leu Ala Asp Lys Leu Ser Glu Ala Gly Lys Ser Val
275 280 285

Leu Leu Ile Glu Lys Gly Pro Pro Ser Ser Gly Arg Trp Gly Gly Thr
290 295 300

Leu Lys Pro Glu Trp Leu Lys Asp Thr Asn Leu Thr Arg Phe Asp Val
305 310 315 320

Pro Gly Leu Cys Asn Gln Ile Trp Val Asn Ser Ala Gly Val Ala Cys
325 330 335

Thr Asp Thr Asp Gln Met Ala Gly Cys Val Leu Gly Gly Gly Thr Ala
340 345 350

Val Asn Ala Gly Leu Trp Trp Lys Pro Tyr Asn Leu Asp Trp Asp Tyr
355 360 365

Asn Phe Pro Arg Gly Trp Lys Ser Arg Asp Met Ala Ala Ala Thr Arg
370 375 380

```
Arg Val Phe Ser Arg Ile Pro Gly Thr Asp Asn Pro Ser Met Asp Gly
385                 390                 395                 400

Lys Arg Tyr Leu Gln Gln Gly Phe Glu Ile Leu Ala Gly Gly Leu Lys
                405                 410                 415

Ala Ala Gly Trp Thr Glu Val Thr Ala Asn Asp Ala Pro Asn Lys Lys
            420                 425                 430

Asn His Thr Tyr Ser His Ser Pro Phe Met Phe Ser Gly Gly Glu Arg
        435                 440                 445

Gly Gly Pro Met Gly Thr Tyr Leu Val Ser Ala Ser Arg Arg Lys Asn
    450                 455                 460

Phe His Leu Trp Thr Gly Thr Ala Val Lys Arg Val Val Arg Thr Gly
465                 470                 475                 480

Gly His Ile Thr Gly Leu Glu Val Glu Pro Phe Val Asn Gly Gly Tyr
                485                 490                 495

Thr Gly Val Val Asn Val Thr Ser Ile Thr Gly Arg Val Val Leu Ser
            500                 505                 510

Ala Gly Ala Phe Gly Ser Ala Lys Ile Leu Leu Arg Ser Gly Ile Gly
        515                 520                 525

Pro Glu Asp Gln Leu Glu Ile Val Lys Ser Ser Thr Asp Gly Pro Thr
    530                 535                 540

Met Ile Ser Asp Ser Ser Trp Ile Thr Leu Pro Val Gly Tyr Asn Leu
545                 550                 555                 560

Glu Asp His Thr Asn Thr Asp Thr Val Val Thr His Pro Asp Val Val
                565                 570                 575

Phe Tyr Asp Phe Tyr Glu Ala Gly His Pro Asn Val Thr Asp Lys Asp
            580                 585                 590

Leu Tyr Leu Asn Ser Arg Ala Gly Ile Leu Ala Gln Ala Ala Pro Asn
        595                 600                 605

Ile Gly Pro Met Phe Trp Glu Glu Ile Lys Gly Arg Asp Gly Val Val
    610                 615                 620

Arg Gln Leu Gln Trp Thr Ala Arg Val Glu Gly Ser Ala Gly Thr Pro
625                 630                 635                 640

Asn Gly Tyr Ala Met Thr Met Ser Gln Tyr Leu Gly Arg Gly Ala Lys
                645                 650                 655

Ser Arg Gly Arg Met Thr Ile Thr Lys Ala Leu Thr Thr Val Val Ser
```

660 665 670

Thr Val Pro Tyr Leu Gln Asp Lys Asn Asp Val Glu Ala Val Ile Gln
675 680 685

Gly Ile Lys Asn Leu Gln Ala Ala Leu Ser Asn Val Lys Asn Leu Thr
690 695 700

Trp Ala Tyr Pro Pro Ser Asn Thr Thr Val Glu Asp Phe Val Asn Asn
705 710 715 720

Met Leu Val Ser Tyr Thr Asn Arg Arg Ser Asn His Trp Ile Gly Thr
725 730 735

Asn Lys Leu Gly Thr Asp Asp Gly Arg Ser Arg Gly Gly Ser Ala Val
740 745 750

Val Asp Leu Asn Thr Lys Val Tyr Gly Thr Asp Asn Leu Phe Val Val
755 760 765

Asp Ala Gly Ile Phe Pro Gly His Ile Thr Thr Asn Pro Thr Ser Tyr
770 775 780

Ile Val Ile Ala Ala Glu Arg Ala Ser Glu Arg Ile Leu Asp Leu Pro
785 790 795 800

Pro Ala Arg Ala Gln Pro Arg Phe Ala Gln Cys Gly Gly Arg Thr Trp
805 810 815

Thr Gly Ser Phe Gln Cys Ala Ala Pro Tyr Thr Cys Gln Tyr Arg Asn
820 825 830

Glu Arg Tyr Ser Gln Cys Arg
835

<210> 4
<211> 2520
<212> DNA
<213> H. haematostroma

<400> 4
atgggtcgcc taggctctct cgcgaagttg cttctcgcag tcggcttgaa tgttcagcaa 60

tgcttcgggc aaaacggacc cccgaccccc tacactgata gtgagaccgg tatcactttc 120

gccacctggt ccggcggaaa cggcttagca ccctggggcg gcttgacttt cggtgttgcg 180

ttacctgaaa atgccctgac caccgacgct accgagctga ttggatacct gaaatgcggt 240

tccaatggca caaccacaga tgcgtggtgt ggtctgtcgt ttgggggccc gatgactaac 300

agcctccttc tcatggcctg gccgcacgaa gacgagatct tgacatcatt ccgttttgcc 360

agtggatata ccagaccaga cctatacacc ggcgatgcca aattaacgca gatatcatcc 420

accatcgata aagatcactt tactctaatt ttcaggtgcc agaactgtct agcgtggaac 480

caagacggcg cgtctggttc cgcttcaact agtgccggct ccttgatatt aggctgggcc 540

agtgcgcttc gggccccgac gaatgcaggc tgtccggctg aaatcaactt caacttccac 600

aacaatggcc agatgatatg gggcgctaca ttagacgaga gcgccgcaaa cccatcatat 660

tcggaatggg ctgccaaagc caccgctacg gttaccggtg actgcggcgg tgcaacccct 720

acgaccacta ctaccaccac cacgtccgtc cctaccgcca caggtatccc agtgccaact 780

ggcacctacg actatattgt agttggtgcg ggtgctggcg gaataccttt ggccgacaag 840

ctgagcgagg ctggaaagag tgtgttactg atcgaaaagg ggccgccatc atcgggacga 900

tggggtggca ccctcaagcc agagtggttg aaggacacca acttgacacg gtttgacgtc 960

cctggcctgt gcaatcagat ctgggtcaac tctgcaggcg tcgcttgtac tgacacagac 1020

caaatggccg gttgcgttct tggtggtggt acagctgtca acgctggcct atggtggaag 1080

ccctacaacc tcgactggga ttataacttc ccacgcggat ggaagtccag ggatatggcc 1140

gctgcaacca ggagagtctt ctctcgcatt cccggtacag ataatccctc aatggatggc 1200

aagcggtatt tacagcaagg cttcgaaatc ctcgctggtg gcttgaaagc cgctggatgg 1260

accgaggtta ccgcgaatga cgcacccaat aagaagaacc acacctactc acactcgccg 1320

ttcatgttct ccggcggcga acggggtggc ccaatgggca cctacctggt atcggccagt 1380

agacgtaaga atttccatct atggacggga acagcagtga agagggttgt tcgcacaggc 1440

ggccatatca ccggtctgga ggtcgagccc ttcgtaaacg gcggttatac cggtgttgtc 1500

aacgtcacct cgattactgg tcgggtcgtc ttgtctgctg gtgcgttcgg gtcggctaag 1560

atattactga ggagcggcat cggacctgag gatcagttgg agattgtcaa gtcatcaacc 1620

gatggcccga ccatgatttc cgattcttct tggattacgc tacccgtcgg ttataatcta 1680

gaggatcaca caaacaccga cacggtcgtt acgcatcctg acgtcgtatt ttacgacttc 1740

tacgaggctg gacatcctaa tgttaccgac aaggacttgt atctcaactc acgggccgga 1800

atccttgctc aagcagcgcc taatatcggc ccaatgttct gggaagagat taagggtagg 1860

gacggcgtcg ttagacagct ccagtggaca gccagagttg aaggaagtgc cggtacaccg 1920

aatgggtacg ccatgacaat gagccaatac cttggacgag gcgctaagtc gaggggccga 1980

atgactatca cgaaggcgtt gacgaccgtc gtttctacag taccttacct acaggataag 2040

aacgacgtgg aagcagtcat ccagggaatc aagaaccttc aagcagcact ttcgaacgtg 2100

aagaatctca catgggccta cccaccatct aatacgacgg tggaggactt tgttaacaac 2160

atgctggttt catacactaa taggcgttcc aaccactgga ttgggaccaa caagctcgga 2220

accgatgatg gccgatcgcg cggaggttca gctgtcgtgg acctcaacac taaggtatac 2280

ggcaccgaca acctgttcgt cgttgacgca ggaatattcc ccggtcatat taccacgaac 2340

ccgacttcgt atatcgtgat cgccgctgag cgcgcttctg agaggatcct cgaccttccc 2400

ccggctagag cacaaccgcg cttcgcgcag tgcggcgggc gaacgtggac gggtagcttc 2460

cagtgtgcag cgccgtacac ttgtcagtac aggaatgagc ggtattccca gtgccggtaa 2520

<210> 5
<211> 831

<212> PRT
<213> C. attrobruneum

<400> 5

```
Met Arg Pro Ser Ser Arg Phe Val Gly Ala Leu Ala Ala Ala Ala Ser
1               5                  10                  15

Phe Leu Pro Ser Ala Leu Ala Gln Asn Asn Ala Ala Val Thr Phe Thr
            20                  25                  30

Asp Pro Asp Thr Gly Ile Val Phe Asn Ser Trp Gly Leu Ala Asn Gly
        35                  40                  45

Ala Pro Gln Thr Gln Gly Gly Phe Thr Phe Gly Val Ala Leu Pro Ser
    50                  55                  60

Asp Ala Leu Thr Thr Asp Ala Thr Glu Phe Ile Gly Tyr Leu Glu Cys
65                  70                  75                  80

Ala Ser Ala Asp Asn Gln Gly Trp Cys Gly Val Ser Met Gly Gly Pro
                85                  90                  95

Met Thr Asn Ser Leu Leu Ile Thr Ala Trp Pro His Glu Asp Asn Val
            100                 105                 110

Tyr Thr Ser Leu Arg Phe Ala Thr Gly Tyr Ala Met Pro Asp Val Tyr
        115                 120                 125

Ser Gly Asp Ala Thr Ile Thr Gln Ile Ser Ser Ser Ile Asn Ala Thr
    130                 135                 140

His Phe Lys Leu Ile Phe Arg Cys Gln Asn Cys Leu Gln Trp Thr His
145                 150                 155                 160

Asp Gly Ala Ser Gly Gly Ala Ser Thr Ser Ala Gly Val Leu Val Leu
                165                 170                 175

Gly Trp Val Gln Ala Phe Pro Ser Pro Gly Asn Pro Thr Cys Pro Asp
            180                 185                 190

Gln Ile Thr Leu Glu Gln His Asn Asn Gly Met Gly Ile Trp Gly Ala
        195                 200                 205

Val Met Asp Ser Asn Val Ala Asn Pro Ser Tyr Thr Glu Trp Ala Ala
    210                 215                 220

Gln Ala Thr Lys Thr Val Glu Ala Glu Cys Asp Gly Pro Ser Glu Thr
225                 230                 235                 240

Asp Ile Val Gly Val Pro Val Pro Thr Gly Thr Thr Phe Asp Tyr Ile
                245                 250                 255

Val Val Gly Gly Gly Ala Gly Gly Ile Pro Thr Ala Asp Lys Leu Ser
```

260 265 270

Glu Ala Gly Lys Ser Val Leu Leu Ile Glu Lys Gly Ile Ala Ser Thr
275 280 285

Ala Glu His Gly Gly Thr Leu Gly Pro Glu Trp Leu Glu Gly Asn Asp
290 295 300

Leu Thr Arg Phe Asp Val Pro Gly Leu Cys Asn Gln Ile Trp Val Asp
305 310 315 320

Ser Lys Gly Ile Ala Cys Glu Asp Thr Asp Gln Met Ala Gly Cys Val
325 330 335

Leu Gly Gly Gly Thr Ala Val Asn Ala Gly Leu Trp Phe Lys Pro Tyr
340 345 350

Ser Leu Asp Trp Asp Tyr Leu Phe Pro Ser Gly Trp Lys Tyr Arg Asp
355 360 365

Ile Gln Ala Ala Ile Gly Arg Val Phe Ser Arg Ile Pro Gly Thr Asp
370 375 380

Ala Pro Ser Thr Asp Gly Lys Arg Tyr Tyr Gln Gln Gly Phe Asp Val
385 390 395 400

Leu Ala Gly Gly Leu Ser Ala Gly Gly Trp Asn Lys Val Thr Ala Asn
405 410 415

Ser Ser Pro Asp Lys Lys Asn Arg Thr Phe Ser Asn Ala Pro Phe Met
420 425 430

Phe Ser Gly Gly Glu Arg Gly Gly Pro Leu Ala Thr Tyr Leu Thr Ser
435 440 445

Ala Lys Lys Arg Ser Asn Phe Asn Leu Trp Leu Asn Thr Ser Val Lys
450 455 460

Arg Val Ile Arg Glu Gly Gly His Val Thr Gly Val Glu Val Glu Pro
465 470 475 480

Phe Arg Thr Gly Gly Tyr Gln Gly Ile Val Asn Val Thr Ala Val Ser
485 490 495

Gly Arg Val Val Leu Ser Ala Gly Thr Phe Gly Ser Ala Lys Ile Leu
500 505 510

Leu Arg Gly Gly Ile Gly Pro Ala Asp Gln Leu Glu Val Val Lys Ala
515 520 525

Ser Lys Ile Asp Gly Pro Thr Met Ile Ser Asn Ala Ser Trp Ile Pro
530 535 540

```
Leu Pro Val Gly Tyr Asn Leu Asp Asp His Leu Asn Thr Asp Thr Val
545                 550                 555                 560

Ile Thr His Pro Asp Val Ala Phe Tyr Asp Phe Tyr Glu Ala Trp Asn
                565                 570                 575

Thr Pro Ile Glu Ala Asp Lys Asn Ser Tyr Leu Ser Ser Arg Thr Gly
            580                 585                 590

Ile Leu Ala Gln Ala Ala Pro Asn Ile Gly Pro Met Met Trp Glu Glu
        595                 600                 605

Ile Lys Gly Ala Asp Gly Ile Val Arg Gln Leu Gln Trp Thr Ala Arg
    610                 615                 620

Val Glu Gly Ser Phe Asp Thr Pro Asn Gly Gln Ala Met Thr Ile Ser
625                 630                 635                 640

Gln Tyr Leu Gly Arg Gly Ala Thr Ser Arg Gly Arg Met Thr Ile Thr
                645                 650                 655

Pro Ser Leu Thr Thr Val Val Ser Asp Val Pro Tyr Leu Lys Asp Pro
            660                 665                 670

Asn Asp Lys Glu Ala Val Ile Gln Gly Ile Val Asn Leu Gln Asn Ala
        675                 680                 685

Leu Lys Asn Val Ala Gly Leu Thr Trp Thr Tyr Pro Asn Ser Ser Ile
    690                 695                 700

Thr Pro Arg Glu Tyr Val Asp Asn Met Val Val Ser Pro Ser Asn Arg
705                 710                 715                 720

Arg Ala Asn His Trp Met Gly Thr Ala Lys Ile Gly Thr Asp Asp Gly
                725                 730                 735

Arg Leu Ala Gly Gly Ser Ala Val Val Asp Leu Asn Thr Lys Val Tyr
            740                 745                 750

Gly Thr Asp Asn Leu Phe Val Val Asp Ala Ser Ile Phe Pro Gly Thr
        755                 760                 765

Pro Thr Thr Asn Pro Ser Ala Tyr Ile Val Thr Ala Ala Glu His Ala
    770                 775                 780

Ser Gln Arg Ile Leu Gly Leu Ala Ala Pro Lys Pro Val Gly Lys Trp
785                 790                 795                 800

Gly Gln Cys Gly Gly Arg Gln Trp Thr Gly Ser Phe Gln Cys Val Ser
                805                 810                 815

Gly Thr Lys Cys Glu Val Val Asn Glu Trp Tyr Ser Gln Cys Leu
```

820 825 830

<210> 6
<211> 2496
<212> DNA
<213> C. attrobruneum

<400> 6

atgaggccct cctctcggtt tgttggtgcc ctggcggcgg cggcgtcgtt cctgccgtct 60
gcccttgccc agaacaatgc tgcagtcacc ttcactgacc cggacaccgg catcgtcttc 120
aactcctggg gtcttgccaa tggagcacca cagactcagg gaggcttcac ctttggtgtc 180
gctctgccct ctgatgcgct cacgaccgat gctaccgagt tcattggtta tttggaatgt 240
gcctccgcgg acaaccaggg ctggtgcggt gtctcgatgg gcggccccat gaccaactcg 300
cttcttatca ccgcctggcc gcacgaggac aacgtctaca cctccctccg gtttgcaaca 360
ggatacgcca tgccggatgt ctactcggga gacgccacca tcacgcagat ctcgtcgagc 420
atcaacgcga cccacttcaa gctcatcttc aggtgccaga actgcctgca atggacccac 480
gacggcgctt ccggtggcgc ctccacgtct gccggtgttc tggtcctcgg ctgggtccag 540
gctttccctt cccctggcaa cccgacgtgc ccggaccaga tcacgctcga gcagcacaac 600
aacggcatgg gcatctgggg tgcggtgatg gactccaacg tcgccaaccc gtcctacaca 660
gagtgggccg cgcaggccac caagacggtc gaggccgagt gcgacggccc gagtgagacg 720
gatattgtcg gcgtgcccgt gccgaccggc accaccttcg actacatcgt cgtgggcggc 780
ggtgccggcg gtatccccac tgccgacaag ctcagcgagg ccggcaagag tgtgctgctg 840
attgagaagg gcatcgcctc gactgctgag cacggcggca ctctcggacc cgagtggctc 900
gagggcaacg acctgacgcg gttcgacgtg cccggtcttt gcaaccagat ctgggttgac 960
tccaagggca tcgcctgcga ggacaccgac cagatggccg gttgcgtcct cggcggcggc 1020
acggccgtca acgccggcct ctggttcaag ccctactcgc tcgactggga ctacctcttc 1080
ccaagcggct ggaagtaccg cgacatccag gccgccatcg gcagggtgtt ctcgcgcatc 1140
ccgggcactg acgcgccctc gaccgacggc aagcgctact accagcaggg cttcgacgtg 1200
ctcgcgggcg gcctgagtgc cggcggctgg aacaaggtca cggccaactc gtctccagac 1260
aagaagaacc gcaccttctc gaacgcgcct ttcatgttct cgggcggcga gcgcggcggg 1320
cccctggcca cttatctcac cagcgccaag aagcgcagca acttcaacct gtggctcaac 1380
acgtcggtca agcgcgtcat ccgtgagggc ggccacgtca caggtgtcga ggtcgagcct 1440
ttccggacgg gcgggtacca gggtatcgtg aacgttaccg ccgtttcggg ccgtgtcgtc 1500
ctgtcggctg gtaccttcgg cagtgccaag attctgctca gaggcggtat tggcccagcg 1560
gatcagctcg aggttgtcaa ggcgtcgaag atcgacgggc cgaccatgat cagcaatgcg 1620
tcttggattc ctctgcctgt tgggtacaac ctggatgacc atctcaacac tgacactgtc 1680
attacccacc ccgacgttgc cttctacgac ttctacgagg catggaacac gcccattgag 1740
gcggacaaga acagctacct gagcagccgc actggtatcc tcgctcaggc cgcgcccaac 1800
attggcccaa tgatgtggga ggaaatcaag ggtgccgacg gtatcgtccg ccagctgcaa 1860

tggaccgccc gtgtcgaggg tagctttgac acgcctaacg ggcaggcgat gaccatctcg 1920

cagtacctcg gccgcggcgc gacctcgcgc ggccgtatga ccatcacccc ttcgctgacg 1980

accgtcgtct cggacgtgcc gtacctcaag gacccgaacg ataaggaggc cgtcatccag 2040

ggcatcgtca acctgcagaa cgccctcaaa aacgtcgccg gcctgacctg gacctacccc 2100

aactcgagca tcacaccgcg cgaatacgtc gataatatgg tagtctcccc tagcaaccgg 2160

cgcgcaaacc actggatggg cacggccaaa atcggcaccg acgacggccg cctggccggc 2220

ggctccgccg tcgtggactt gaacaccaag gtctacggca ccgacaacct ctttgtcgtg 2280

gacgcgtcca tcttccccgg cacgcccacc accaatccct cggcgtacat cgtcacggct 2340

gcggagcatg cttcgcagag gatcttgggg ttggctgcgc cgaagccggt tgggaaatgg 2400

ggccagtgtg gcgggcggca gtggacaggg agcttccagt gcgtgagtgg gacaaagtgt 2460

gaggtggtga atgagtggta ctcgcagtgc ttgtag 2496

<210> 7
<211> 787
<212> PRT
<213> C. thermophilum

<400> 7

Met Lys Leu Leu Ser Arg Val Gly Ala Thr Ala Leu Ala Ala Thr Leu
1 5 10 15

Ser Leu Lys Gln Cys Ala Ala Gln Met Thr Glu Gly Thr Tyr Thr His
20 25 30

Glu Ala Thr Gly Ile Thr Phe Lys Thr Trp Thr Pro Ser Asp Gly Ser
35 40 45

Thr Phe Thr Phe Gly Leu Ala Leu Pro Gly Asp Ala Leu Thr Asn Asp
50 55 60

Ala Thr Glu Tyr Ile Gly Leu Leu Arg Cys Gln Ile Thr Asp Pro Ser
65 70 75 80

Ser Pro Gly Tyr Cys Gly Ile Ser His Gly Gln Ser Gly Gln Met Thr
85 90 95

Gln Ala Leu Leu Leu Val Ala Trp Ala Ser Glu Asp Val Val Tyr Thr
100 105 110

Ser Phe Arg Tyr Ala Thr Gly Tyr Thr Leu Pro Glu Leu Tyr Thr Gly
115 120 125

Asp Ala Lys Leu Thr Gln Ile Ala Ser Ser Val Ser Gly Asp Ser Phe
130 135 140

Glu Val Leu Phe Arg Cys Glu Asn Cys Phe Ser Trp Asp Gln Asn Gly
145 150 155 160

```
Ala Thr Gly Ser Val Ser Thr Ser Asn Gly Ala Leu Val Leu Gly Tyr
                165                 170                 175

Ala Ala Ser Lys Ser Gly Leu Thr Gly Ala Thr Cys Pro Asp Thr Ala
            180                 185                 190

Glu Phe Gly Phe His Asn Asn Gly Phe Gly Gln Trp Gly Ala Val Leu
        195                 200                 205

Glu Gly Ala Thr Ser Asp Ser Tyr Glu Glu Trp Ala Gln Leu Ala Thr
    210                 215                 220

Ile Thr Pro Pro Thr Thr Cys Asp Gly Asn Gly Pro Gly Asp Lys Val
225                 230                 235                 240

Cys Val Pro Ala Pro Glu Asp Thr Tyr Asp Tyr Ile Val Val Gly Ala
                245                 250                 255

Gly Ala Gly Gly Ile Thr Val Ala Asp Lys Leu Ser Glu Ala Gly His
            260                 265                 270

Lys Val Leu Leu Ile Glu Lys Gly Pro Pro Ser Thr Gly Leu Trp Asn
        275                 280                 285

Gly Thr Met Lys Pro Glu Trp Leu Glu Gly Thr Asp Leu Thr Arg Phe
    290                 295                 300

Asp Val Pro Gly Leu Cys Asn Gln Ile Trp Val Asp Ser Ala Gly Ile
305                 310                 315                 320

Ala Cys Thr Asp Thr Asp Gln Met Ala Gly Cys Val Leu Gly Gly Gly
                325                 330                 335

Thr Ala Val Asn Ala Gly Leu Trp Trp Lys Pro His Pro Ala Asp Trp
            340                 345                 350

Asp Asp Asn Phe Pro His Gly Trp Lys Ser Ser Asp Leu Ala Asp Ala
        355                 360                 365

Thr Glu Arg Val Phe Ser Arg Ile Pro Gly Thr Trp His Pro Ser Gln
    370                 375                 380

Asp Gly Lys Leu Tyr Arg Gln Glu Gly Phe Glu Val Ile Ser Gln Gly
385                 390                 395                 400

Leu Ala Asn Ala Gly Trp Arg Glu Val Asp Ala Asn Gln Glu Pro Ser
                405                 410                 415

Glu Lys Asn Arg Thr Tyr Ser His Ser Val Phe Met Phe Ser Gly Gly
            420                 425                 430

Glu Arg Gly Gly Pro Leu Ala Thr Tyr Leu Ala Ser Ala Ala Gln Arg
```

435 440 445

Ser Asn Phe Asn Leu Trp Val Asn Thr Ser Val Arg Arg Ala Ile Arg
450 455 460

Thr Gly Pro Arg Val Ser Gly Val Glu Leu Glu Cys Leu Ala Asp Gly
465 470 475 480

Gly Phe Asn Gly Thr Val Asn Leu Lys Glu Gly Gly Gly Val Ile Phe
485 490 495

Ser Ala Gly Ala Phe Gly Ser Ala Lys Leu Leu Leu Arg Ser Gly Ile
500 505 510

Gly Pro Glu Asp Gln Leu Glu Ile Val Ala Ser Ser Lys Asp Gly Glu
515 520 525

Thr Phe Ile Ser Lys Asn Asp Trp Ile Lys Leu Pro Val Gly His Asn
530 535 540

Leu Ile Asp His Leu Asn Thr Asp Leu Ile Ile Thr His Pro Asp Val
545 550 555 560

Val Phe Tyr Asp Phe Tyr Ala Ala Trp Asp Asn Pro Ile Thr Glu Asp
565 570 575

Lys Glu Ala Tyr Leu Asn Ser Arg Ser Gly Ile Leu Ala Gln Ala Ala
580 585 590

Pro Asn Ile Gly Pro Leu Met Trp Glu Glu Val Thr Pro Ser Asp Gly
595 600 605

Ile Thr Arg Gln Phe Gln Trp Thr Cys Arg Val Glu Gly Asp Ser Ser
610 615 620

Lys Thr Asn Ser Thr His Ala Met Thr Leu Ser Gln Tyr Leu Gly Arg
625 630 635 640

Gly Val Val Ser Arg Gly Arg Met Gly Ile Thr Ser Gly Leu Thr Thr
645 650 655

Thr Val Ala Glu His Pro Tyr Leu His Asn Asp Gly Asp Leu Glu Ala
660 665 670

Val Ile Gln Gly Ile Gln Asn Val Val Asp Ala Leu Ser Gln Val Pro
675 680 685

Asp Leu Glu Trp Val Leu Pro Pro Pro Asn Thr Thr Val Glu Glu Tyr
690 695 700

Val Asn Ser Leu Ile Val Ser Pro Ala Asn Arg Arg Ala Asn His Trp
705 710 715 720

Met Gly Thr Ala Lys Met Gly Leu Asp Asp Gly Arg Ser Gly Gly Ser
725 730 735

Ala Val Val Asp Leu Asn Thr Lys Val Tyr Gly Thr Asp Asn Leu Phe
740 745 750

Val Val Asp Ala Ser Ile Phe Pro Gly Met Ser Thr Gly Asn Pro Ser
755 760 765

Ala Met Ile Val Ile Val Ala Glu Gln Ala Ala Gln Arg Ile Leu Ser
770 775 780

Leu Arg Tyr
785

<210> 8
<211> 2364
<212> DNA
<213> C. thermophilum

<400> 8
atgaagcttc tcagccgcgt tggggccacc gccctagcgg cgacgttgtc cctgaaacaa 60

tgtgcagctc agatgaccga agggacgtac acccatgagg ctaccggtat cacgttcaag 120

acatggactc cttccgacgg ctcgactttc actttcggct tggccctccc tggggacgcg 180

ctgacaaatg atgccaccga gtacattggt ctcctgcgtt gccaaatcac cgatccctct 240

tcgcccggct actgtggcat ctcccacggc cagtccggcc agatgacgca ggcgctgctg 300

ctggtcgctt gggccagcga ggatgtcgtc tacacgtcgt tccgctacgc caccggctac 360

acactccccg agctctacac gggcgacgcc aagctgaccc agatcgcctc ctcggtcagc 420

ggggacagct tcgaggtgct gttccgctgc gagaactgct tctcctggga ccagaacggc 480

gccacgggca gtgtctcgac cagcaacggc gccctggttc tcggctacgc tgcctcgaag 540

agtggtttga cgggcgccac gtgcccggac acggccgagt ttggcttcca caacaatggt 600

ttcggacagt ggggtgcagt gctcgagggt gcgacctcgg actcgtatga ggagtgggct 660

cagctggcca ctatcacgcc cccgaccacc tgcgatggca acggccctgg cgacaaggtg 720

tgcgttccgg ctcccgaaga cacgtatgat tacatcgttg tcggcgccgg cgccggcggc 780

atcacggtcg ccgacaagct cagcgaggcc ggccacaagg tcctccttat cgagaagggt 840

cctccgtcga ccggcctgtg gaacgggacc atgaagcccg agtggctcga gggtaccgac 900

ctcacccgct tcgacgtccc cggtctgtgc aaccagatct gggtcgactc tgccggcatt 960

gcctgcaccg ataccgacca gatggcgggc tgcgttctcg gcggtggcac cgctgtcaat 1020

gctggtctgt ggtggaagcc ccaccccgct gactgggacg acaacttccc tcatggctgg 1080

aagtcgagcg atctcgcgga tgcgaccgag cgtgtcttca gccgcattcc cggcacgtgg 1140

cacccgtcgc aggatggcaa actgtaccgc caggagggct tcgaggtcat cagccagggc 1200

ctggccaacg ccggctggag ggaagtcgac gccaaccagg agcccagcga gaagaaccgc 1260

acgtattccc acagtgtgtt catgttctcg ggcggtgagc gcggcggccc cctggcgacg 1320

tacctcgcct cggctgccca gcgcagcaac ttcaacttgt gggtcaacac ttcggtccgg 1380

agggccatcc gcaccggccc cagggtcagt ggcgtcgaac tcgagtgcct tgcggacggc 1440

ggcttcaacg gtactgtcaa cctgaaggag ggtggtggtg tcatcttttc ggctggcgct 1500

ttcggctcgg ccaagctgct ccttcgcagc ggcatcggtc ctgaggacca gctcgagatt 1560

gtggcgagct ccaaggacgg cgagaccttc atttccaaga atgattggat caagctcccc 1620

gtcggccata acctgatcga tcatctcaac accgacctca ttattactca cccggatgtc 1680

gttttctatg acttctacgc ggcttgggac aatcccatca ccgaggacaa ggaggcctac 1740

ctgaactcgc ggtccggcat tctcgcccaa gcggcgccca acatcggccc tctgatgtgg 1800

gaggaagtca cgccatccga cggcatcacc cgccagttcc agtggacatg ccgtgttgag 1860

ggcgacagct ccaagaccaa ctcgacccac gccatgaccc tcagccagta tctcggccgt 1920

ggcgtcgtct cgcgcggccg gatgggcatc acttccgggc tgaccacgac ggtggccgag 1980

cacccgtacc tgcacaacga cggcgacctg gaggcggtga tccagggtat ccagaacgtg 2040

gtggacgcgc tcagccaggt gcccgacctc gagtgggtgc tcccgccgcc caacacgacg 2100

gtggaggaat acgtcaacag cctgatcgtg tctccggcta accgccgggc caaccactgg 2160

atgggcacgg ccaagatggg cctcgatgac ggccgctcgg gcggctccgc ggtcgtcgac 2220

ctcaacacaa aggtgtatgg caccgacaac ctgtttgtcg tcgacgcctc catcttccct 2280

ggcatgtcga cgggcaaccc gtcggctatg atcgtcatcg tggccgagca ggcggcccag 2340

cgcatcctgt ccctgcggta ttag 2364

<210> 9
<211> 829
<212> PRT
<213> S. bisbyi

<400> 9

Met Leu Phe Lys Leu Ser Asn Trp Leu Leu Ala Leu Ala Leu Phe Val
1 5 10 15

Gly Asn Val Val Ala Gln Leu Glu Gly Pro Thr Pro Tyr Thr Asp Pro
20 25 30

Asp Thr Gly Ile Val Phe Gln Ser Trp Val Asn Pro Ala Gly Thr Leu
35 40 45

Lys Phe Gly Tyr Thr Tyr Pro Ala Asn Ala Ala Thr Val Ala Ala Thr
50 55 60

Glu Phe Ile Gly Phe Leu Glu Cys Gln Gly Ala Gly Trp Cys Ser Val
65 70 75 80

Ser Leu Gly Gly Ser Met Leu Asn Lys Pro Leu Val Val Ala Tyr Pro
85 90 95

Ser Gly Asp Glu Val Leu Ala Ser Leu Lys Trp Ala Thr Gly Tyr Ala

100 105 110

Asn Pro Glu Pro Tyr Gly Gly Asn His Lys Leu Ser Gln Ile Ser Ser
115 120 125

Ser Val Thr Ser Ala Gly Phe Arg Val Val Tyr Arg Cys Glu Gly Cys
130 135 140

Leu Ala Trp Asn Tyr Gln Gly Ile Glu Gly Gly Ser Pro Thr Asn Gly
145 150 155 160

Ala Ser Met Pro Ile Gly Trp Ala Tyr Ser Ala Ser Ser Val Leu Asn
165 170 175

Gly Asp Cys Val Asp Asn Thr Val Leu Ile Gln His Asp Thr Phe Gly
180 185 190

Asn Tyr Gly Phe Val Pro Asp Glu Ser Ser Leu Arg Thr Glu Tyr Asn
195 200 205

Asp Trp Thr Glu Leu Pro Thr Arg Val Val Arg Gly Asp Cys Gly Gly
210 215 220

Ser Thr Thr Thr Ser Ser Val Pro Ser Ser Thr Ala Pro Pro Gln Gly
225 230 235 240

Thr Gly Ile Pro Val Pro Thr Gly Ala Ser Tyr Asp Tyr Ile Val Val
245 250 255

Gly Ser Gly Ala Gly Gly Ile Pro Ile Ala Asp Lys Leu Thr Glu Ala
260 265 270

Gly Lys Lys Val Leu Leu Ile Glu Lys Gly Pro Pro Ser Ser Gly Arg
275 280 285

Tyr Asp Gly Lys Leu Lys Pro Thr Trp Leu Glu Gly Thr Asn Leu Thr
290 295 300

Arg Phe Asp Val Pro Gly Leu Cys Asn Gln Ile Trp Val Asp Ser Ala
305 310 315 320

Gly Ile Ala Cys Arg Asp Thr Asp Gln Met Ala Gly Cys Val Leu Gly
325 330 335

Gly Gly Thr Ala Val Asn Ala Gly Leu Trp Trp Lys Pro Asn Pro Ile
340 345 350

Asp Trp Asp Tyr Asn Phe Pro Ser Gly Trp Lys Ser Ser Glu Met Ile
355 360 365

Gly Ala Thr Asn Arg Val Phe Ser Arg Ile Gly Gly Thr Thr Val Pro
370 375 380

Ser Gln Asp Gly Lys Thr Tyr Tyr Gln Gln Gly Phe Asn Val Leu Ser
385 390 395 400

Ser Gly Leu Lys Ala Ala Gly Trp Thr Ser Val Ser Leu Asn Asn Ala
405 410 415

Pro Ala Gln Arg Asn Arg Thr Tyr Gly Ala Gly Pro Phe Met Phe Ser
420 425 430

Gly Gly Glu Arg Gly Gly Pro Leu Ala Thr Tyr Leu Ala Thr Ala Lys
435 440 445

Lys Arg Gly Asn Phe Asp Leu Trp Thr Asn Thr Gln Val Lys Arg Val
450 455 460

Ile Arg Gln Gly Gly His Val Thr Gly Val Glu Val Glu Asn Tyr Asn
465 470 475 480

Gly Asp Gly Tyr Lys Gly Thr Val Lys Val Thr Pro Val Ser Gly Arg
485 490 495

Val Val Leu Ser Ala Gly Thr Phe Gly Ser Ala Lys Leu Leu Leu Arg
500 505 510

Ser Gly Ile Gly Pro Lys Asp Gln Leu Ala Ile Val Lys Asn Ser Thr
515 520 525

Asp Gly Pro Thr Met Ala Ser Glu Arg Asp Trp Ile Asn Leu Pro Val
530 535 540

Gly Tyr Asn Leu Glu Asp His Thr Asn Thr Asp Ile Val Ile Ser His
545 550 555 560

Pro Asp Val Val His Tyr Asp Phe Tyr Glu Ala Trp Thr Ala Ser Ile
565 570 575

Glu Ser Asp Lys Thr Ala Tyr Leu Gly Lys Arg Ser Gly Ile Leu Ala
580 585 590

Gln Ala Ala Pro Asn Ile Gly Pro Leu Phe Phe Asp Glu Val Arg Gly
595 600 605

Ala Asp Asn Ile Val Arg Ser Ile Gln Tyr Thr Ala Arg Val Glu Gly
610 615 620

Asn Ser Val Val Pro Asn Gly Lys Ala Met Val Ile Ser Gln Tyr Leu
625 630 635 640

Gly Arg Gly Ala Val Ser Arg Gly Arg Met Thr Ile Ser Gln Gly Leu
645 650 655

Asn Thr Ile Val Ser Thr Ala Pro Tyr Leu Ser Asn Val Asn Asp Leu

660 665 670

Glu Ala Val Ile Lys Ser Leu Glu Asn Ile Ala Asn Ser Leu Thr Ser
675 680 685

Lys Val Lys Asn Leu Lys Ile Glu Trp Pro Ala Ser Gly Thr Ser Ile
690 695 700

Arg Asp His Val Thr Asn Met Pro Leu Asp Pro Ala Thr Arg Arg Ala
705 710 715 720

Asn His Trp Ile Gly Thr Asn Lys Ile Gly Thr Lys Asn Gly Arg Leu
725 730 735

Thr Gly Gly Asp Ser Val Val Asp Leu Asn Thr Lys Val Tyr Gly Thr
740 745 750

Asp Asn Leu Phe Val Val Asp Ala Ser Ile Phe Pro Gly Met Val Thr
755 760 765

Thr Asn Pro Ser Ala Tyr Ile Val Ile Ala Ala Glu His Ala Ala Ser
770 775 780

Lys Ile Leu Ser Leu Pro Thr Ala Lys Ala Ala Ala Lys Tyr Glu Gln
785 790 795 800

Cys Gly Gly Leu Glu Tyr Asn Gly Asn Phe Gln Cys Ala Ser Gly Leu
805 810 815

Thr Cys Thr Trp Leu Asn Asp Tyr Tyr Trp Gln Cys Thr
820 825

<210> 10
<211> 2490
<212> DNA
<213> S. bisbyi

<400> 10
atgctgttca agctctcaaa ttggttgcta gcgcttgcgc tctttgttgg caatgtcgtt 60

gctcaactcg aggggcctac cccgtacacg gatccagata ccggcattgt ctttcagtcc 120

tgggtcaatc cagcagggac cctgaagttt ggttacactt accccgcaaa tgctgctacg 180

gttgccgcca cggaatttat cggtttcctg gaatgccaag gggctggatg gtgtagcgtc 240

tcactcggtg gctccatgct taacaagccg cttgttgttg cctaccctag tggcgatgaa 300

gtcctcgctt ctttgaagtg ggccacaggc tacgcgaatc cagagcctta cggcggcaat 360

cacaagctgt cccagatcag ctcgtccgtc acctctgctg gcttcagggt cgtctatcga 420

tgtgagggat gtctcgcctg gaactaccag ggaattgagg gagggagccc caccaatggt 480

gcgtccatgc ctatcggttg ggcttacagc gcaagttctg tactcaacgg ggattgtgtg 540

gataacactg ttctcattca acatgacacc tttggcaatt atggcttcgt acctgatgaa 600

tcatctcttc gcacggagta caatgactgg acggagcttc cgaccagggt tgtcagggga 660

gactgcggcg gttccacaac tacctcttcg gtgccctcct caacggcgcc tcctcaaggt 720
actggcatac cggttcctac tggcgcaagc tatgactaca tagttgttgg ctcgggtgct 780
ggaggtattc ccattgcgga taagcttacc gaggctggca aaaaggtttt gttgattgag 840
aagggaccac cctcttctgg tcgctacgat ggaaagctaa agccgacgtg gcttgaggga 900
actaatctca cccgattcga tgtgcctggc ctctgcaacc aaatatgggt cgactccgct 960
ggcattgcat gccgtgatac cgatcagatg gctggttgtg ttcttggcgg tggtactgct 1020
gtcaatgcag gtctatggtg gaagcctaac cctattgatt gggactataa tttcccttca 1080
ggctggaagt caagcgagat gataggcgcg acaaaccgtg tcttttcacg tattggtggt 1140
actactgttc cttcgcagga cggaaagacc tactatcagc aaggtttcaa cgttctttcc 1200
agcggtctca aggctgcggg ctggacatct gttagcctga ataacgcccc tgcgcaaagg 1260
aaccgcacct atggtgctgg ccctttcatg ttctctggtg gagagcgagg tggacctttg 1320
gccacctacc tggccactgc caagaagaga ggaaacttcg acctctggac gaatacccaa 1380
gttaagcgtg taattcgaca gggaggtcat gttactggag tggaggtcga aaactataac 1440
ggtgatgggt acaagggcac tgtcaaggtg actcctgtat ctgggcgagt tgtcctatct 1500
gctggtacct ttggcagtgc taagcttttg ctccgaagcg gtatcggtcc caaggatcaa 1560
ctagctattg tcaagaactc gactgatggc cctactatgg cttccgagag ggactggatt 1620
aatcttcccg ttggctacaa cttggaggac catactaaca ccgacattgt catctcccat 1680
ccagatgtgg tccattacga cttctatgag gcttggacag cgtcaatcga gtctgacaag 1740
actgcttatt tgggcaagcg ttctggcatc ctcgctcaag ccgcccccaa catcgggcct 1800
ctcttctttg acgaagttcg cggtgctgac aacattgtcc gctcaattca gtacactgct 1860
cgtgtggagg gcaacagtgt ggtccctaat ggcaaggcca tggtgatcag ccagtacctt 1920
ggtcgtggcg ctgtttccag gggtcgaatg accatctctc aaggtctcaa tacgattgtt 1980
tccaccgctc catacctctc aaacgtcaat gatctcgagg ccgtcattaa gagccttgag 2040
aacatagcga acagcttgac gtcaaaggtt aaaaacctca agattgaatg gcctgcctct 2100
ggtacatcca ttcgcgatca cgtcacgaat atgcctctcg acccggccac ccgccgagcg 2160
aatcattgga ttggcactaa caagatcgga accaagaatg gtcgactgac aggtggtgat 2220
tccgtcgttg atttgaacac taaggtctat ggtacagaca atctgtttgt ggtcgatgct 2280
tctattttcc ctggcatggt tacgaccaac ccctcggcct acattgtaat tgccgctgag 2340
catgctgcat cgaagattct gagcctacct actgctaagg ctgccgcgaa gtacgaacaa 2400
tgtggtggcc ttgaatataa tggtaacttt cagtgtgcgt ctggattaac ctgcacttgg 2460
ttaaacgact actactggca gtgtacttaa 2490

<210> 11
<211> 829
<212> PRT
<213> N. crassa

<400> 11

```
Met Arg Thr Thr Ser Ala Phe Leu Ser Gly Leu Ala Ala Val Ala Ser
1               5                  10                  15

Leu Leu Ser Pro Ala Phe Ala Gln Thr Ala Pro Lys Thr Phe Thr His
            20                  25                  30

Pro Asp Thr Gly Ile Val Phe Asn Thr Trp Ser Ala Ser Asp Ser Gln
        35                  40                  45

Thr Lys Gly Gly Phe Thr Val Gly Met Ala Leu Pro Ser Asn Ala Leu
    50                  55                  60

Thr Thr Asp Ala Thr Glu Phe Ile Gly Tyr Leu Glu Cys Ser Ser Ala
65                  70                  75                  80

Lys Asn Gly Ala Asn Ser Gly Trp Cys Gly Val Ser Leu Arg Gly Ala
                85                  90                  95

Met Thr Asn Asn Leu Leu Ile Thr Ala Trp Pro Ser Asp Gly Glu Val
            100                 105                 110

Tyr Thr Asn Leu Met Phe Ala Thr Gly Tyr Ala Met Pro Lys Asn Tyr
        115                 120                 125

Ala Gly Asp Ala Lys Ile Thr Gln Ile Ala Ser Ser Val Asn Ala Thr
    130                 135                 140

His Phe Thr Leu Val Phe Arg Cys Gln Asn Cys Leu Ser Trp Asp Gln
145                 150                 155                 160

Asp Gly Val Thr Gly Gly Ile Ser Thr Ser Asn Lys Gly Ala Gln Leu
                165                 170                 175

Gly Trp Val Gln Ala Phe Pro Ser Pro Gly Asn Pro Thr Cys Pro Thr
            180                 185                 190

Gln Ile Thr Leu Ser Gln His Asp Asn Gly Met Gly Gln Trp Gly Ala
        195                 200                 205

Ala Phe Asp Ser Asn Ile Ala Asn Pro Ser Tyr Thr Ala Trp Ala Ala
    210                 215                 220

Lys Ala Thr Lys Thr Val Thr Gly Thr Cys Ser Gly Pro Val Thr Thr
225                 230                 235                 240

Ser Ile Ala Ala Thr Pro Val Pro Thr Gly Val Ser Phe Asp Tyr Ile
                245                 250                 255

Val Val Gly Gly Gly Ala Gly Gly Ile Pro Val Ala Asp Lys Leu Ser
            260                 265                 270

Glu Ser Gly Lys Ser Val Leu Leu Ile Glu Lys Gly Phe Ala Ser Thr
```

```
          275                 280                 285

Gly Glu His Gly Gly Thr Leu Lys Pro Glu Trp Leu Asn Asn Thr Ser
 290                 295                 300

Leu Thr Arg Phe Asp Val Pro Gly Leu Cys Asn Gln Ile Trp Lys Asp
305                 310                 315                 320

Ser Asp Gly Ile Ala Cys Ser Asp Thr Asp Gln Met Ala Gly Cys Val
                325                 330                 335

Leu Gly Gly Gly Thr Ala Ile Asn Ala Gly Leu Trp Tyr Lys Pro Tyr
            340                 345                 350

Thr Lys Asp Trp Asp Tyr Leu Phe Pro Ser Gly Trp Lys Gly Ser Asp
        355                 360                 365

Ile Ala Gly Ala Thr Ser Arg Ala Leu Ser Arg Ile Pro Gly Thr Thr
 370                 375                 380

Thr Pro Ser Gln Asp Gly Lys Arg Tyr Leu Gln Gln Gly Phe Glu Val
385                 390                 395                 400

Leu Ala Asn Gly Leu Lys Ala Ser Gly Trp Lys Glu Val Asp Ser Leu
                405                 410                 415

Lys Asp Ser Glu Gln Lys Asn Arg Thr Phe Ser His Thr Ser Tyr Met
            420                 425                 430

Tyr Ile Asn Gly Glu Arg Gly Gly Pro Leu Ala Thr Tyr Leu Val Ser
        435                 440                 445

Ala Lys Lys Arg Ser Asn Phe Lys Leu Trp Leu Asn Thr Ala Val Lys
 450                 455                 460

Arg Val Ile Arg Glu Gly Gly His Ile Thr Gly Val Glu Val Glu Ala
465                 470                 475                 480

Phe Arg Asn Gly Gly Tyr Ser Gly Ile Ile Pro Val Thr Asn Thr Thr
                485                 490                 495

Gly Arg Val Val Leu Ser Ala Gly Thr Phe Gly Ser Ala Lys Ile Leu
            500                 505                 510

Leu Arg Ser Gly Ile Gly Pro Lys Asp Gln Leu Glu Val Val Lys Ala
        515                 520                 525

Ser Ala Asp Gly Pro Thr Met Val Ser Asn Ser Ser Trp Ile Asp Leu
 530                 535                 540

Pro Val Gly His Asn Leu Val Asp His Thr Asn Thr Asp Thr Val Ile
545                 550                 555                 560
```

Gln His Asn Asn Val Thr Phe Tyr Asp Phe Tyr Lys Ala Trp Asp Asn
565 570 575

Pro Asn Thr Thr Asp Met Asn Leu Tyr Leu Asn Gly Arg Ser Gly Ile
580 585 590

Phe Ala Gln Ala Ala Pro Asn Ile Gly Pro Leu Phe Trp Glu Glu Ile
595 600 605

Thr Gly Ala Asp Gly Ile Val Arg Gln Leu His Trp Thr Ala Arg Val
610 615 620

Glu Gly Ser Phe Glu Thr Pro Asp Gly Tyr Ala Met Thr Met Ser Gln
625 630 635 640

Tyr Leu Gly Arg Gly Ala Thr Ser Arg Gly Arg Met Thr Leu Ser Pro
645 650 655

Thr Leu Asn Thr Val Val Ser Asp Leu Pro Tyr Leu Lys Asp Pro Asn
660 665 670

Asp Lys Ala Ala Val Val Gln Gly Ile Val Asn Leu Gln Lys Ala Leu
675 680 685

Ala Asn Val Lys Gly Leu Thr Trp Ala Tyr Pro Ser Ala Asn Gln Thr
690 695 700

Ala Ala Asp Phe Val Asp Lys Gln Pro Val Thr Tyr Gln Ser Arg Arg
705 710 715 720

Ser Asn His Trp Met Gly Thr Asn Lys Met Gly Thr Asp Asp Gly Arg
725 730 735

Ser Gly Gly Thr Ala Val Val Asp Thr Asn Thr Arg Val Tyr Gly Thr
740 745 750

Asp Asn Leu Tyr Val Val Asp Ala Ser Ile Phe Pro Gly Val Pro Thr
755 760 765

Thr Asn Pro Thr Ala Tyr Ile Val Val Ala Ala Glu His Ala Ala Ala
770 775 780

Lys Ile Leu Ala Gln Pro Ala Asn Glu Ala Val Pro Lys Trp Gly Trp
785 790 795 800

Cys Gly Gly Pro Thr Tyr Thr Gly Ser Gln Thr Cys Gln Ala Pro Tyr
805 810 815

Lys Cys Glu Lys Gln Asn Asp Trp Tyr Trp Gln Cys Val
820 825

<210> 12

<211> 2490
<212> DNA
<213> N. crassa

<400> 12

atgaggacca cctcggcctt tctcagcggc ctggcggcgg tggcttcatt gctgtcgccc 60

gccttcgccc aaaccgctcc caagaccttc actcatcctg ataccggcat tgtcttcaac 120

acatggagtg cttccgattc ccagaccaaa ggtggcttca ctgttggtat ggctctgccg 180

tcaaatgctc ttactaccga cgcgactgaa ttcatcggtt atctggaatg ctcctccgcc 240

aagaatggtg ccaatagcgg ttggtgcggt gtttctctca gaggcgccat gaccaacaat 300

ctactcatta ccgcctggcc ttctgacgga gaagtctaca ccaatctcat gttcgccacg 360

ggttacgcca tgcccaagaa ctacgctggt gacgccaaga tcacccagat cgcgtccagc 420

gtgaacgcta cccacttcac ccttgtcttt aggtgccaga actgtttgtc atgggaccaa 480

gacggtgtca ccggcggcat ttctaccagc aataaggggg cccagctcgg ttgggtccag 540

gcgttcccct ctcccggcaa cccgacttgc cctacccaga tcactctcag tcagcatgac 600

aacggtatgg gccagtgggg agctgccttt gacagcaaca ttgccaatcc ctcttatact 660

gcatgggctg ccaaggccac caagaccgtt accggtactt gcagtggtcc agtcacgacc 720

agtattgccg ccactcctgt tcccactggc gtttcttttg actacattgt cgttggtggt 780

ggtgccggtg gtattcccgt cgctgacaag ctcagcgagt ccggtaagag cgtgctgctc 840

atcgagaagg gtttcgcttc cactggtgag catggtggta ctctgaagcc cgagtggctg 900

aataatacat cccttactcg cttcgatgtt cccggtcttt gcaaccagat ctggaaagac 960

tcggatggca ttgcctgctc cgataccgat cagatggccg gctgcgtgct cggcggtggt 1020

accgccatca acgccggtct ctggtacaag ccctacacca aggactggga ctacctcttc 1080

ccctctggct ggaagggcag cgatatcgcc ggtgctacca gcagagccct ctcccgcatt 1140

ccgggtacca ccactccttc tcaggatgga aagcgctacc ttcagcaggg tttcgaggtt 1200

cttgccaacg gcctcaaggc gagcggctgg aaggaggtcg attccctcaa ggacagcgag 1260

cagaagaacc gcactttctc ccacacctca tacatgtaca tcaatggcga gcgtggcggt 1320

cctctagcga cttacctcgt cagcgccaag aagcgcagca acttcaagct gtggctcaac 1380

accgctgtca agcgcgtcat ccgtgagggc ggccacatta ccggtgtgga ggttgaggcc 1440

ttccgcaacg gcggctactc cggaatcatc cccgtcacca acaccaccgg ccgcgtcgtt 1500

ctttccgccg gcaccttcgg cagcgccaag atccttctcc gttccggcat tggccccaag 1560

gaccagctcg aggtggtcaa ggcctccgcc gacggcccta ccatggtcag caactcgtcc 1620

tggattgacc tccccgtcgg ccacaacctg gttgaccaca ccaacaccga caccgtcatc 1680

cagcacaaca acgtgacctt ctacgacttt tacaaggctt gggacaaccc caacacgacc 1740

gacatgaacc tgtacctcaa tgggcgctcc ggcatcttcg cccaggccgc gcccaacatt 1800

ggcccccttgt tctgggagga gatcacgggc gccgacggca tcgtccgtca gctgcactgg 1860

accgcccgcg tcgagggcag cttcgagacc cccgacggct acgccatgac catgagccag 1920

taccttggcc gtggcgccac ctcgcgcggc cgcatgaccc tcagccctac cctcaacacc 1980

gtcgtgtctg acctcccgta cctcaaggac cccaacgaca aggccgctgt cgttcagggt 2040

atcgtcaacc tccagaaggc tctcgccaac gtcaagggtc tcacctgggc ttaccctagc 2100

gccaaccaga cggctgctga ttttgttgac aagcaacccg taacctacca atcccgccgc 2160

tccaaccact ggatgggcac caacaagatg ggcaccgacg acggccgcag cggcggcacc 2220

gcagtcgtcg acaccaacac gcgcgtctat ggcaccgaca acctgtacgt ggtggacgcc 2280

tcgattttcc ccggtgtgcc gaccaccaac cctaccgcct acattgtcgt cgccgctgag 2340

catgccgcgg ccaaaatcct ggcgcaaccc gccaacgagg ccgttcccaa gtggggctgg 2400

tgcggcgggc cgacgtatac tggcagccag acgtgccagg cgccatataa gtgcgagaag 2460

cagaatgatt ggtattggca gtgtgtgtag 2490

<210> 13
<211> 34
<212> DNA
<213> artificial

<220>
<223> anchor primer

<400> 13
ggccacgcgt cgactagtac ttttttttt tttt 34

<210> 14
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 14
atgcctctct tgtttggacc g 21

<210> 15
<211> 22
<212> DNA
<213> artificial

<220>
<223> primer

<400> 15
tcaactctca tacttggctt gg 22

<210> 16
<211> 19
<212> DNA
<213> artificial

<220>
<223> primer

<400> 16
tagagtcgag gcgaaccag 19

<210> 17
<211> 20

<212> DNA
<213> artificial

<220>
<223> primer

<400> 17
ttgctgctgt gctcctatgc 20

<210> 18
<211> 23
<212> DNA
<213> artificial

<220>
<223> primer

<400> 18
tcttgctacg cacttcggta ttg 23

<210> 19
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 19
tgtgtaccct gtttactcac c 21

<210> 20
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer

<400> 20
tcttataagc ctttggctcc 20

<210> 21
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer

<400> 21
ttggctccgt tggaacaatg 20

<210> 22
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer

<400> 22
cgcaccaacc gtgtgaagtg 20

<210> 23
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 23
tacaagatga ggaccacctc g 21

<210> 24
<211> 22
<212> DNA
<213> artificial

<220>
<223> primer

<400> 24
tacatccagc ttaccggcac tg 22

<210> 25
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 25
ttccttccct ccatcaactc c 21

<210> 26
<211> 23
<212> DNA
<213> artificial

<220>
<223> primer

<400> 26
gtacccatta agtacactgc cag 23

<210> 27
<211> 20
<212> DNA
<213> artificial

<220>
<223> primer

<400> 27
ttccccccttc gaattcggtc 20

<210> 28
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 28
agctacctat caccctctgt c 21

<210> 29
<211> 26
<212> DNA
<213> artificial

<220>
<223> primer

<400> 29
tccaagcttt taaagatcca ggtaac 26

<210> 30
<211> 21
<212> DNA
<213> artificial

<220>
<223> primer

<400> 30
aaaagcttgg acccaaccaa g 21

<210> 31
<211> 31
<212> DNA
<213> artificial

<220>
<223> primer

<400> 31
gtcttctatt ctttttactc tgcttgggat g 31

<210> 32
<211> 19
<212> DNA
<213> artificial

<220>
<223> primer

<400> 32
atagaagacc acatcaggg 19

Claims

1. A cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above, selected from a cellobiose dehydrogenase being a modified cellobiose dehydrogenase of *Myriococcum thermophilum,* a cellobiose dehydrogenase isolated from *Chaetomium atrobrunneum, Hypoxylon haematostroma or Stachybotrys bisbyi.*

2. Cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprising an amino acid sequence of SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 9 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to SEQ ID NO: 3, SEQ ID NO: 5 or SEQ ID NO: 9.

3. Cellobiose dehydrogenase according to claim 1 being a modified cellobiose dehydrogenase of *Myriococcum thermophilum,* comprising a flavin and a haem domain, wherein electron transfer from the flavin to the haem domain is increased as compared to wild type cellobiose dehydrogenase of *Myriococcum thermophilum,* preferably as measured by the cyt c assay.

4. Cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprising an amino acid sequence of amino acids 22 to 828 of SEQ ID NO: 1 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to amino acids 22 to 828 of SEQ ID NO: 1, **characterised in that** the amino acid sequence has at least one additional amino acid substitution, deletion or insertion to the sequence of SEQ ID NO:1 increasing electron transfer from the flavin to the haem domain as compared to wild type cellobiose dehydrogenase of *Myriococcum thermophilum* of SEQ ID NO:1, preferably as measured by the cyt c assay.

5. Cellobiose dehydrogenase according to claim 4, **characterised in that** the modification is a modification of the haem domain of any one of amino acids 90-100, 115-124, 172-203, preferably of any one of amino acids 176, 179-182, 195, 196, 198, 201 corresponding to the *M. thermophilum* CDH of SEQ ID NO: 1 and/or of the flavin domain of any one of amino acids 311-333, 565-577, 623-625, 653-664, 696-723, preferably of any one of amino acids 318, 325, 326, 328, 568, 571, 574, 575, 624, 654, 663, 702, 709, 712, 717, correspond to the *M. thermophilum* cellobiose dehydrogenase of SEQ ID NO: 1, or any combination thereof, preferably comprising a modification with an increase of positive charge in the of amino acids 172-203 corresponding to the *M. thermophilum* cellobiose dehydrogenase of SEQ ID NO: 1, preferably of amino acid 181, in particular preferred a D181K mutation, and/or a decrease of a negative charge of amino acids 565-577 corresponding to the *M. thermophilum* cellobiose dehydrogenase of SEQ ID NO: 1, preferably of amino acid(s) 568 and/or 571, in particular preferred a D568S and/or E571S mutation, or any combination thereof.

6. Cellobiose dehydrogenase according to any one of claims 1 to 5, being isolated by diafiltration, ion exchange chromatography by collecting fractions with cellobiose dehydrogenase activity, preferably being further purified by hydrophobic interaction chromatography.

7. A nucleic acid molecule encoding a cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above and comprising

- a nucleotide sequence of SEQ ID NOs 4, 6, 8, 10 or 12, or
- the open reading frame of SEQ ID NOs 4, 6, 8, 10 or 12 or
- a nucleotide sequence with at least 50%, preferably at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 98%, in particular preferred at least 99%, identity to SEQ ID NO: 2, 4, 6, 8, 10 or 12 or the open reading frame of SEQ ID NOs: 2, 4, 6, 8, 10 or 12, further comprising a nucleotide mutation, substitution, deletion or insertion, preferably a codon mutation, substitution, deletion or insertion,
- a nucleotide sequence that hybridizes with any one of SEQ ID NO: 2, 4, 6, 8, 10 or 12 under stringent condition,

preferably encoding a cellobiose dehydrogenase as defined in claims 1 to 6.

8. An electrode comprising an immobilised cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above and having at least 10%, preferably at least 14%, in particular preferred at least 18%, glucose, lactose or cellobiose oxidising activity at a pH of 7.4 as compared to their maximal activity at a lower pH as determined by a cyt c assay, preferably also as compared to their maximal activity at a lower pH as determined by a DCIP assay.

9. Electrode according to claim 8, **characterised in that** the glucose oxidation activity at pH 7.4 is at least 0.5 U/mg cellobiose dehydrogenase.

10. Electrode according to any one of claims 8 or 9, **characterised in that** the K_M value of the cellobiose dehydrogenase for an glucose oxidation reaction at pH 7.4 is below 1 M.

11. Electrode according to any one of claims 8 to 10, **characterised in that** the cellobiose dehydrogenase is of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa or Stachybotrys bisbyi* or a modified cellobiose dehydrogenase of *Myriococcum thermophilum* with an increased activity at pH of 7.4 as defined in any one of claims 3 to 5, or the cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprises an amino acid sequence of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11, preferably wherein the cellobiose dehydrogenase is defined as in any one of claims 1 to 6 or encoded by the nucleic acid molecule of claim 7.

12. Electrode according to any one of claims 8 to 11, **characterised in that** the cellobiose dehydrogenase is immobilised by adsorption, complex formation, preferably via an additional complexing linker, covalent or ionic linkage, preferably wherein the immobilized cellobiose dehydrogenase is cross-linked, in particular by bifunctional agents, to increase stability or activity.

13. An electrochemical cell comprising an electrode according to any one of claims 8 to 12 as an anodic element and a cathodic element, preferably comprising a glucose containing solution as anodic fluid, wherein further preferred the anodic fluid is a solution of at least pH 6.0, preferably at least pH 6.5, in particular preferred at least pH 7.0, even more preferred at least pH 7.2 or most preferred at pH 7.4 or above.

14. Method of detecting or quantifying glucose in a sample comprising

- providing a cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above,
- contacting a fluid sample having a pH of at least 6.5, preferably at least 7.0, in particular preferred at least 7.3, especially preferred at least 7.4, with the cellobiose dehydrogenase, and
- detecting an oxidation of glucose of the sample by the cellobiose dehydrogenase,

wherein preferably the oxidation is detected electrochemically, preferably with an immobilised cellobiose dehydrogenase on an electrode, in particular preferred as defined in any one of claims 8 to 12.

15. The method of claim 14, **characterised in that** the cellobiose dehydrogenase is of *Chaetomium atrobrunneum, Corynascus thermophilus, Hypoxylon haematostroma, Neurospora crassa or Stachybotrys bisbyi* or a modified cellobiose dehydrogenase of *Myriococcum thermophilum* with an increased activity at pH of 7.4 as defined in any one of claims 3 to 5,
or the cellobiose dehydrogenase having glucose oxidation activity at a pH of 7.4 or above comprises an amino acid sequence of SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11 or an amino acid sequence being at least 50%, preferably at least 75%, in particular preferred at least 90%, identical to SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 11,
preferably the cellobiose dehydrogenase is further defined as in any one of claims 1 to 6.

Fig. 1

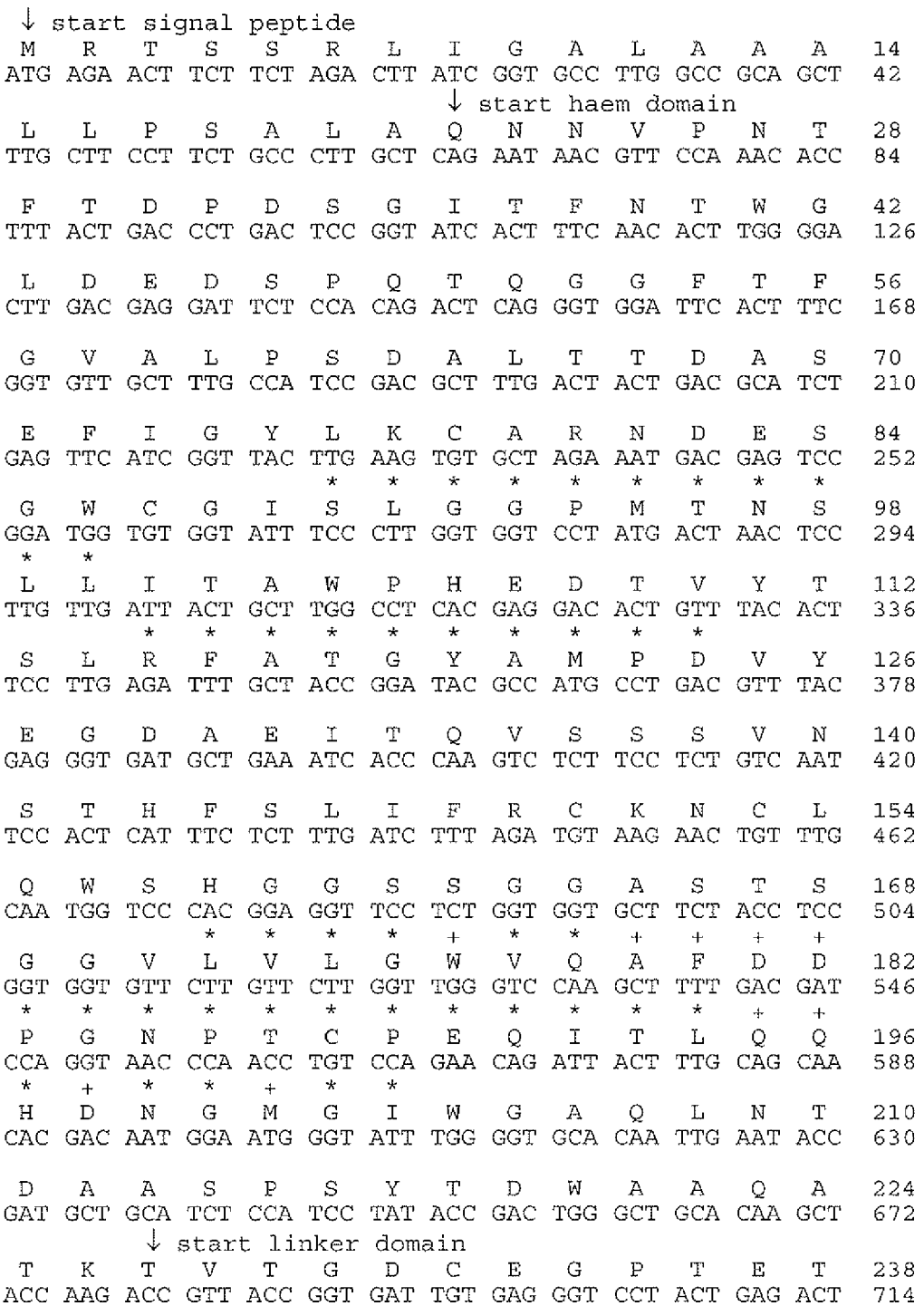
↓ start signal peptide
↓ start haem domain
↓ start linker domain

Fig. 1 Continuation

```
                                                  ↓ start flavin
 S   V   V   G   V   P   V   P   T   G   V   S   F   D   252
TCT GTG GTC GGT GTT CCA GTT CCA ACT GGA GTT TCT TTC GAT   756
domain
 Y   I   V   V   G   G   G   A   G   G   I   P   A   A   266
TAC ATT GTT GTC GGA GGT GGT GCC GGA GGT ATC CCA GCA GCT   798

 D   K   L   S   E   A   G   K   S   V   L   L   I   E   280
GAC AAG CTT TCT GAG GCT GGT AAG TCC GTT TTG CTT ATT GAG   840

 K   G   F   A   S   T   A   N   T   G   G   T   L   G   294
AAG GGT TTC GCT TCT ACC GCT AAT ACC GGA GGT ACT TTG GGT   882

 P   E   W   L   E   G   H   D   L   T   R   F   D   V   308
CCA GAG TGG TTG GAG GGT CAC GAT CTT ACT CGT TTC GAC GTT   924
         *   *   *   *   *   *   *   +   *   *   *   *
 P   G   L   C   N   Q   I   W   V   D   S   K   G   I   322
CCA GGT CTT TGC AAC CAA ATT TGG GTG GAC TCT AAG GGA ATC   966
 *   *   +   +   *   +   *   *   *   *   *
 A   C   E   D   T   D   Q   M   A   G   C   V   L   G   336
GCT TGC GAG GAT ACT GAC CAA ATG GCA GGA TGT GTT CTT GGT  1008

 G   G   T   A   V   N   A   G   L   W   F   K   P   Y   350
GGA GGT ACC GCA GTC AAT GCT GGT CTT TGG TTC AAG CCA TAT  1050

 S   L   D   W   D   Y   L   F   P   D   G   W   K   Y   364
TCT TTG GAT TGG GAT TAC TTG TTT CCT GAC GGT TGG AAG TAC  1092

 N   D   V   Q   P   A   I   N   R   A   L   S   R   I   378
AAC GAC GTC CAA CCT GCC ATC AAC AGA GCT TTG TCT CGT ATT  1134

 P   G   T   D   A   P   S   T   D   G   K   R   Y   Y   392
CCT GGT ACT GAC GCT CCT TCT ACT GAC GGA AAG AGA TAC TAC  1176

 Q   E   G   F   E   V   L   S   K   G   L   A   A   G   406
CAG GAA GGT TTT GAG GTT CTT TCT AAA GGT TTG GCC GCT GGT  1218

 G   W   T   S   V   T   A   N   N   A   P   D   K   K   420
GGA TGG ACC TCT GTG ACT GCA AAC AAT GCT CCA GAC AAG AAG  1260

 N   R   T   F   A   H   A   P   F   M   F   A   G   G   434
AAC CGT ACC TTC GCT CAC GCA CCT TTC ATG TTC GCA GGT GGA  1302

 E   R   N   G   P   L   G   T   Y   F   Q   T   A   K   448
GAG AGA AAC GGT CCA TTG GGT ACC TAC TTT CAA ACT GCC AAA  1344

 K   R   N   N   F   D   V   W   L   N   T   S   V   K   462
AAG CGT AAC AAC TTC GAC GTC TGG CTT AAC ACT TCT GTT AAG  1386

 R   V   I   R   E   G   G   H   I   T   G   V   E   V   476
AGA GTT ATC AGA GAA GGA GGT CAC ATT ACT GGA GTT GAA GTG  1428
```

Fig. 1 Continuation

```
 E   P   F   R   D   G   G   Y   E   G   I   V   P   V   490
GAG CCT TTC AGA GAT GGA GGT TAC GAG GGT ATC GTG CCT GTG  1470
 T   K   V   T   G   R   V   I   L   S   A   G   T   F   504
ACT AAG GTT ACT GGA CGT GTT ATC TTG TCT GCT GGT ACT TTC  1512

 G   S   A   K   I   L   L   R   S   G   I   G   P   E   518
GGT TCC GCC AAG ATT CTT TTG CGT TCC GGT ATT GGA CCA GAG  1554

 D   Q   L   E   V   V   A   A   S   E   K   D   G   P   532
GAC CAA TTG GAG GTC GTT GCC GCT TCT GAG AAG GAT GGA CCT  1596

 T   M   I   G   N   S   S   W   I   N   L   P   V   G   546
ACC ATG ATC GGT AAC TCC TCT TGG ATT AAC TTG CCT GTG GGA  1638

 Y   N   L   D   D   H   L   N   T   D   T   V   I   S   560
TAC AAC TTG GAC GAT CAC TTG AAC ACC GAC ACC GTG ATC TCT  1680
                 *   *   *   +   *   *   +   *   *   +
 H   P   D   V   V   F   Y   D   F   Y   E   A   W   D   574
CAC CCT GAT GTG GTC TTC TAT GAC TTT TAC GAG GCT TGG GAT  1722
+   *   *
 D   P   I   E   S   D   K   N   S   Y   L   E   S   R   588
GAC CCA ATT GAA TCT GAC AAG AAC TCT TAC TTG GAA TCT AGA  1764

 T   G   I   L   A   Q   A   A   P   N   I   G   P   M   602
ACC GGA ATC TTG GCT CAA GCA GCT CCA AAC ATT GGT CCA ATG  1806

 F   W   E   E   I   V   G   A   D   G   I   V   R   Q   616
TTC TGG GAA GAG ATT GTG GGA GCT GAC GGT ATT GTC AGA CAA  1848
                       *   +   *
 L   Q   W   T   A   R   V   E   G   S   L   G   A   P   630
TTG CAG TGG ACC GCC AGA GTT GAG GGT TCT TTG GGT GCA CCT  1890

 N   G   H   T   M   T   M   S   Q   Y   L   G   R   G   644
AAC GGA CAT ACC ATG ACC ATG TCT CAA TAC CTT GGT CGT GGT  1932
                           *   +   *   *   *   +
 A   T   S   R   G   R   M   T   I   T   P   S   L   T   658
GCC ACT TCT AGA GGT AGA ATG ACC ATC ACT CCA TCT TTG ACC  1974
*   *   *   *   +   *
 T   I   V   S   D   V   P   Y   L   K   D   P   N   D   672
ACT ATT GTT TCC GAC GTC CCT TAC CTT AAA GAC CCA AAC GAC  2016

 K   E   A   V   I   Q   G   I   I   N   L   Q   N   A   686
AAA GAA GCC GTG ATT CAA GGT ATT ATC AAC TTG CAG AAT GCT  2058
                               *   *   *   *   *
 L   Q   N   V   A   N   L   T   W   L   F   P   N   S   700
TTG CAG AAC GTT GCC AAT TTG ACC TGG TTG TTC CCA AAC TCT  2100
*   +   *   *   *   *   *   *   +   *   *   +   *   *
 T   I   T   P   R   E   Y   V   E   S   M   V   V   S   714
ACC ATT ACC CCA CGT GAG TAT GTC GAA TCT ATG GTC GTG TCT  2142
*   *   +   *   *   *   *   *   *
 P   S   N   R   R   S   N   H   W   M   G   T   N   K   728
CCT TCT AAC AGA CGT TCT AAC CAC TGG ATG GGT ACT AAC AAA  2184
```

Fig. 1 Continuation

```
 L   G   T   D   D   G   R   K   G   G   S   A   V   V   742
TTG GGT ACT GAT GAC GGT AGA AAA GGT GGA TCC GCA GTG GTT  2226

 D   L   D   T   R   V   Y   G   T   D   N   L   F   V   756
GAC TTG GAC ACT CGT GTC TAT GGT ACC GAT AAC TTG TTC GTT  2268

 I   D   A   S   I   F   P   G   V   P   T   T   N   P   770
ATC GAT GCT TCC ATC TTC CCT GGT GTT CCT ACC ACT AAC CCA  2310

 T   S   Y   I   V   V   A   A   E   H   A   S   S   R   784
ACT TCT TAC ATT GTC GTT GCC GCA GAG CAC GCT TCC TCT CGT  2352

 I   L   A   L   P   D   L   E   P   V   P   K   Y   G   798
ATT CTT GCA TTG CCA GAC CTT GAG CCA GTC CCT AAA TAC GGA  2394

 Q   C   G   G   R   E   W   T   G   S   F   V   C   A   812
CAG TGT GGT GGA AGA GAG TGG ACT GGA TCT TTC GTT TGC GCA  2436

 D   G   S   T   C   E   Y   Q   N   E   W   Y   S   Q   826
GAT GGT TCT ACC TGT GAA TAC CAA AAT GAG TGG TAC TCT CAA  2478

 C   L   *     830
TGT TTG TAA    2490
```

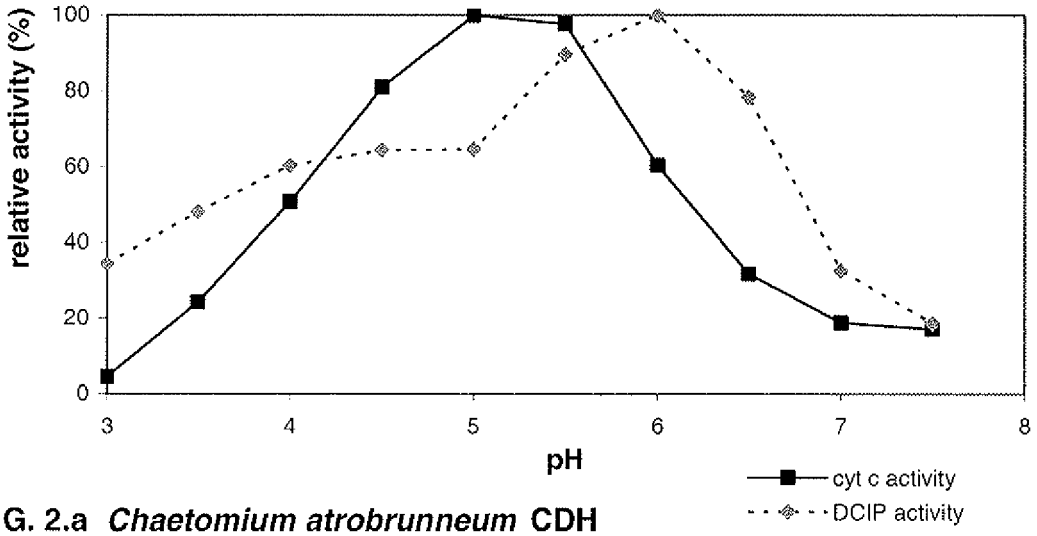

FIG. 2.a *Chaetomium atrobrunneum* CDH

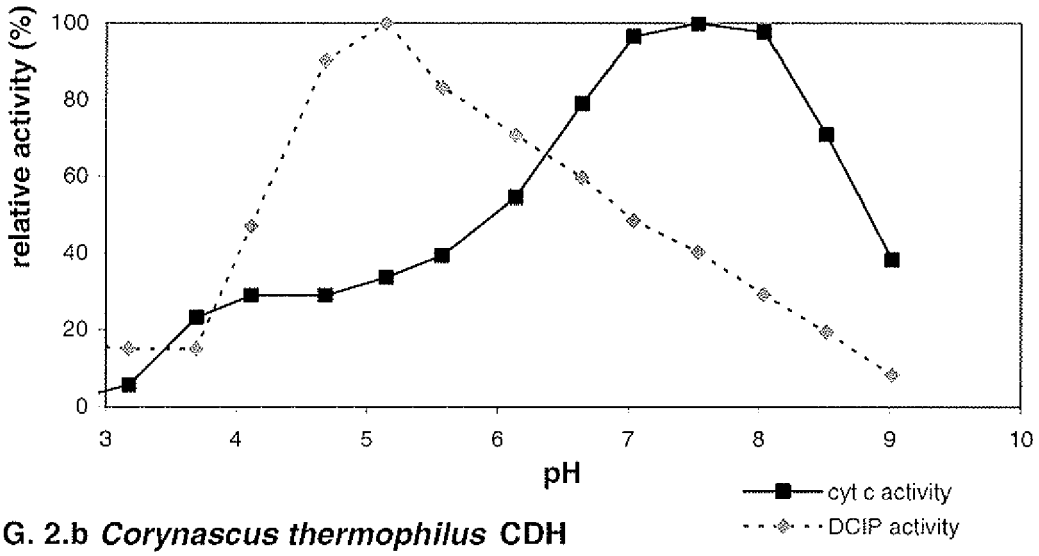

FIG. 2.b *Corynascus thermophilus* CDH

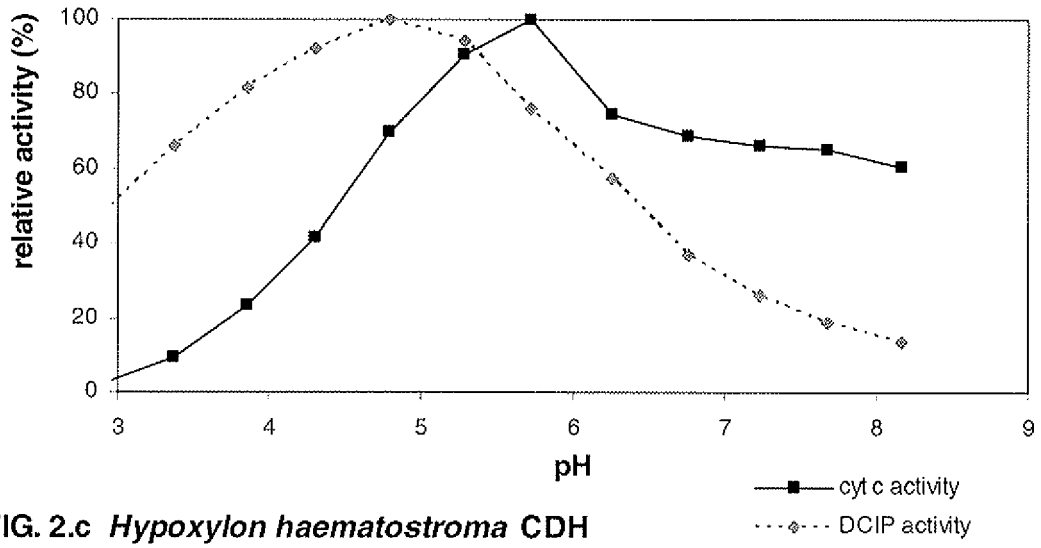

FIG. 2.c *Hypoxylon haematostroma* CDH

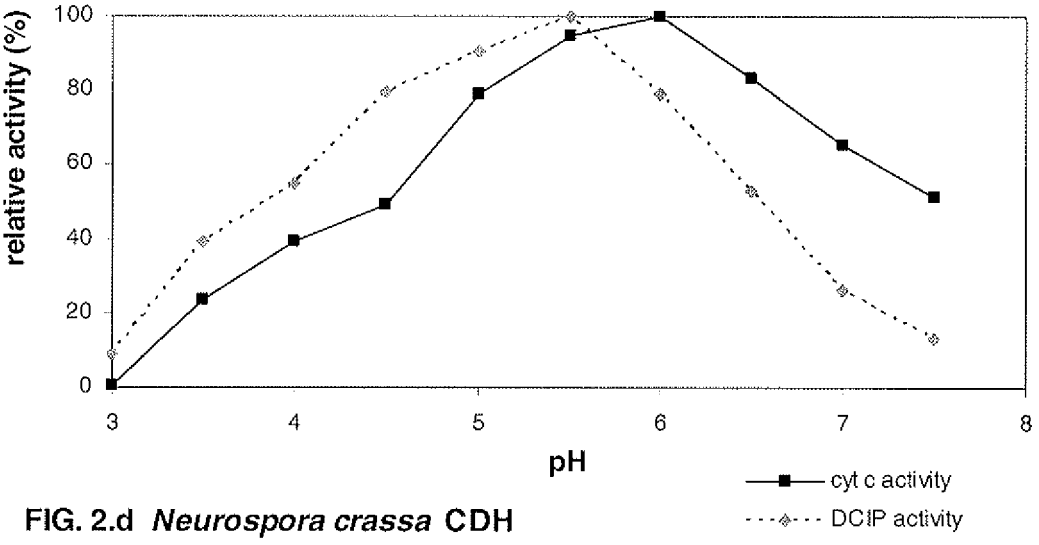

FIG. 2.d *Neurospora crassa* CDH

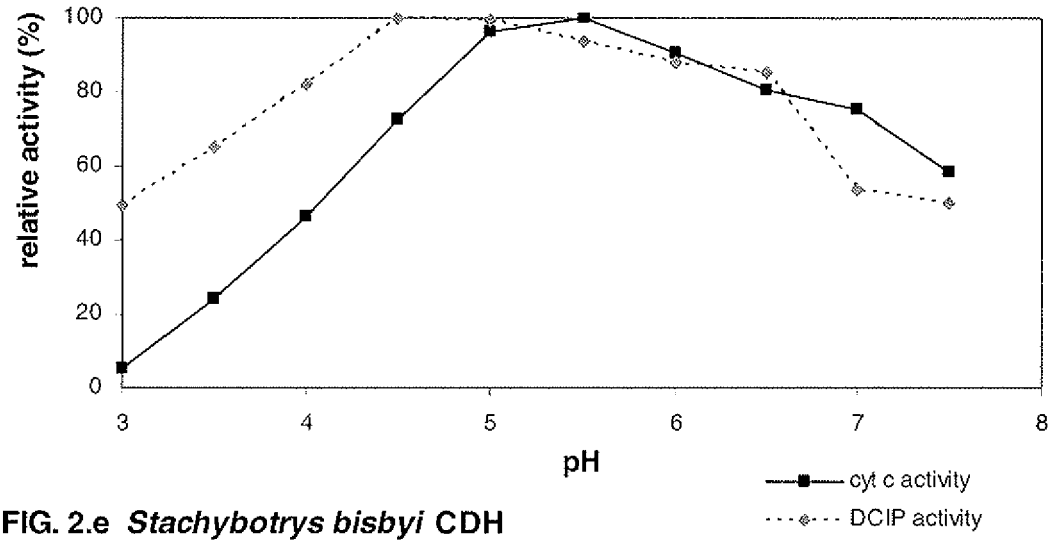

FIG. 2.e *Stachybotrys bisbyi* CDH

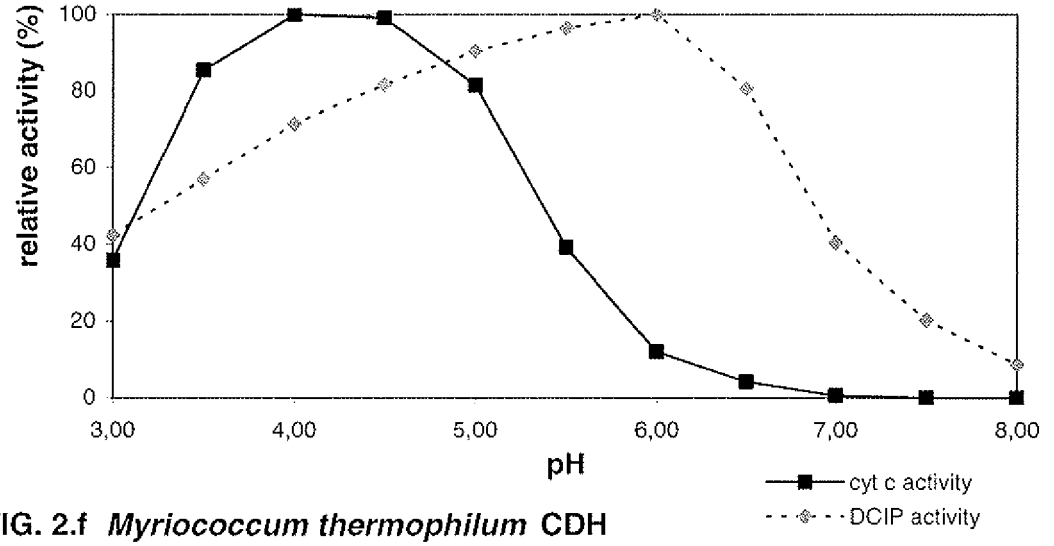

FIG. 2.f *Myriococcum thermophilum* CDH

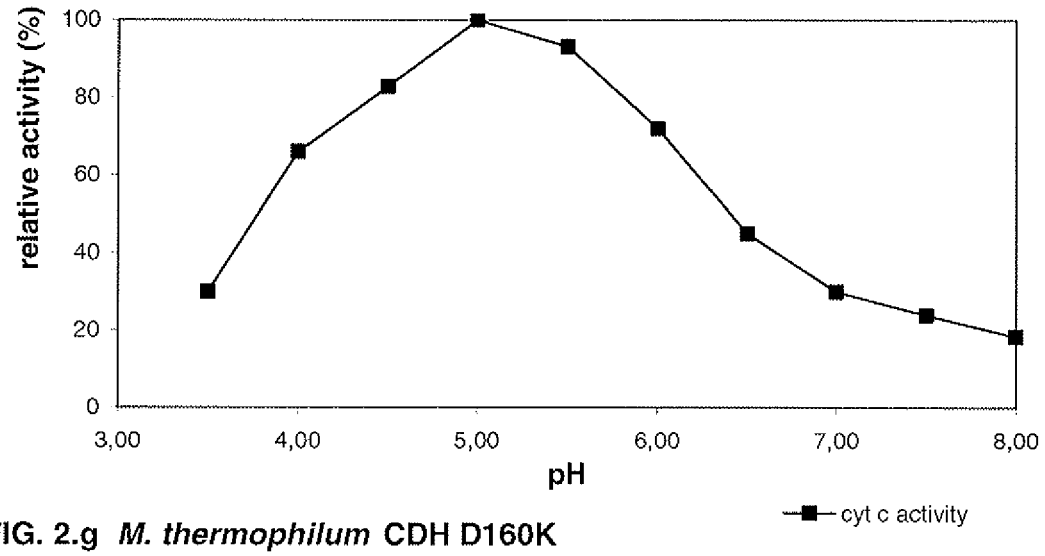

FIG. 2.g *M. thermophilum* CDH D160K

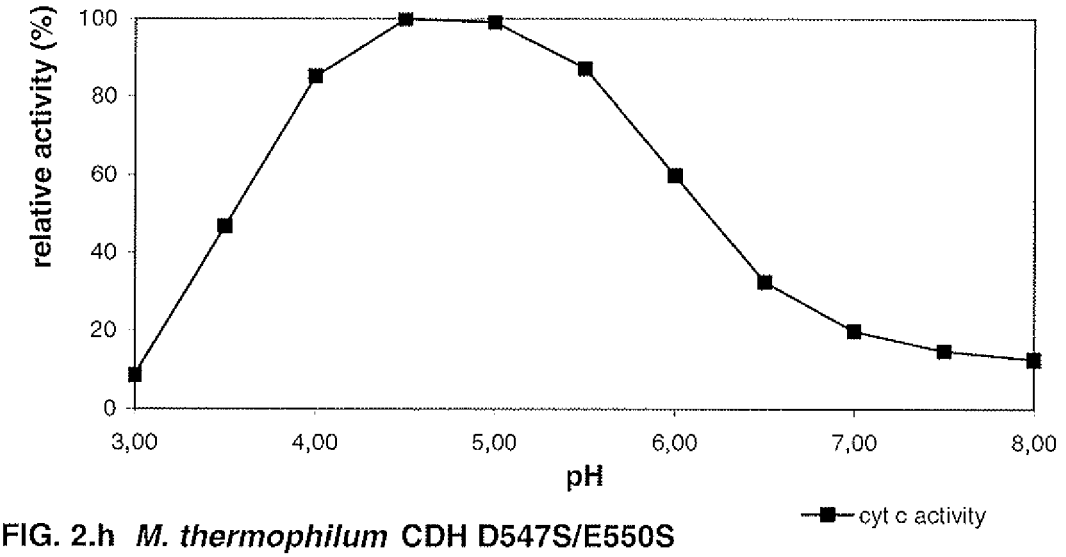

FIG. 2.h *M. thermophilum* CDH D547S/E550S

Fig. 3

```
                  *        20         *        40         *        60         *
C.attro : MRPSSRFVGALAAAASFLPSALAQNNAAVTFTDPDTGIVFNSWGLANGAPQTQGGFTFGVALPSDALTTD :  70
C.therm : MKLLSRVGATALAATLSLKQCAAQM-TEGTYTHEATGITFKTWTPSDG-----STFTFGLALPGDALTND :  64
H.haema : MGRLGSLAKLLLAVGLNVQQCFGQNGPPTPYTDSETGITFATWSGGNG-LAPWGGLTFGVALPENALTTD :  69
M.therm : MRTSSRLIGALAAAL--LPSALAQNNVPNTFTDPDSGITFNTWGLDEDSPQTQGGFTFGVALPSDALTTD :  68
N.crass : MRTTSAFLSGLAAVASLLSPAFAQT-APKTFTHPDTGIVFNTWSASD--SQTKGGFTVGMALPSNALTTD :  67
S.bisby : --MLFKLSNWLLALALFVGNVVAQLEGPTPYTDPDTGIVFQSWVNPAG------TLKFGYTYPANAATVA :  62

                 80         *       100         *       120         *       140
C.attro : ATEFIGYLECASADN---QGWCGVSMG--GPMTNSLLITAWPHEDNVYTSLRFATGYAMPDVYSGDATIT : 135
C.therm : ATEYIGLLRCQITDP-SSPGYCGISHGQSGQMTQALLLVAWASEDVVYTSFRYATGYTLPELYTGDAKLT : 133
H.haema : ATELIGYLKCGSNGT-TTDAWCGLSFG--GPMTNSLLLMAWPHEDEILTSFRFASGYTRPDLYTGDAKLT : 136
M.therm : ASEFIGYLKCARNDE---SGWCGISLG--GPMTNSLLITAWPHEDTVYTSLRFATGYAMPDVYEGDAEIT : 133
N.crass : ATEFIGYLECSSAKNGANSGWCGVSLR--GAMTNNLLITAWPSDGEVYTNLMFATGYAMPKNYAGDAKIT : 135
S.bisby : ATEFIGFLECQ------GAGWCSVSLG--GSMLNKPLVVAYPSGDEVLASLKWATGYANPEPYGGNHKLS : 124

                  *       160         *       180         *       200         *
C.attro : QISSSINATHFKLIFRCQNCLQWTHDGASGGASTSAGVLVLGWVQAFPSPGNPTCPDQITLEQHNNGMGI : 205
C.therm : QIASSVSGDSFEVLFRCENCFSWDQNGATGSVSTSNGALVLGYAASKSGLTGATCPDTAEFGFHNNGFGQ : 203
H.haema : QISSTIDKDHFTLIFRCQNCLAWNQDGASGSASTSAGSLILGWASALRAPTNAGCPAEINFNFHNNGQMI : 206
M.therm : QVSSSVNSTHFSLIFRCKNCLQWSHGGSSGGASTSGGVLVLGWVQAFDDPGNPTCPEQITLQQHDNGMGI : 203
N.crass : QIASSVNATHFTLVFRCQNCLSWDQDGVTGGISTSNKGAQLGWVQAFPSPGNPTCPTQITLSQHDNGMGQ : 205
S.bisby : QISSSVTSAGFRVVYRCEGCLAWNYQGIEGGSPTNGASMPIGWAYSASSVLNGDCVDNTVLIQHDT-FGN : 193

                 220         *       240         *       260         *       280
C.attro : WGAVMDSNVANPSYTEWAAQATKTVEAECDG--PSETDIVGVPVPTGT--------TFDYIVVGGGAGGI : 265
C.therm : WGAVLEG-ATSDSYEEWAQLATITPPTTCDG--NGPGDKVCVPAPEDT---------YDYIVVGAGAGGI : 261
H.haema : WGATLDESAANPSYSEWAAKATATVTGDCGGATPTTTTTTTTSVPTATGIPVPT-GTYDYIVVGAGAGGI : 275
M.therm : WGAQLNTDAASPSYTDWAAQATKTVTGDCEG--PTETSVVGVPVPTGV--------SFDYIVVGGGAGGI : 263
N.crass : WGAAFDSNIANPSYTAWAAKATKTVTGTCSG--PVTTSIAATPVPTGV--------SFDYIVVGGGAGGI : 265
S.bisby : YGFVPDESSLRTEYNDWTELPTRVVRGDCGGSTTTSSVPSSTAPPQGTGIPVPTGASYDYIVVGSGAGGI : 263
```

Fig. 3 Continuation

```
                  *       300         *       320         *       340         *
C.attro : PTADKLSEAGKSVLLIEKGIASTAEHGGTLGPEWLEGNDLTRFDVPGLCNQIWVDSKGIACEDTDQMAGC : 335
C.therm : TVADKLSEAGHKVLLIEKGPPSTGLWNGTMKPEWLEGTDLTRFDVPGLCNQIWVDSAGIACTDTDQMAGC : 331
H.haema : PLADKLSEAGKSVLLIEKGPPSSGRWGGTLKPEWLKDTNLTRFDVPGLCNQIWVNSAGVACTDTDQMAGC : 345
M.therm : PAADKLSEAGKSVLLIEKGFASTANTGGTLGPEWLEGHDLTRFDVPGLCNQIWVDSKGIACEDTDQMAGC : 333
N.crass : PVADKLSESGKSVLLIEKGFASTGEHGGTLKPEWLNNTSLTRFDVPGLCNQIWKDSDGIACSDTDQMAGC : 335
S.bisby : PIADKLTEAGKKVLLIEKGPPSSGRYDGKLKPTWLEGTNLTRFDVPGLCNQIWVDSAGIACRDTDQMAGC : 333

                360         *       380         *       400         *       420
C.attro : VLGGGTAVNAGLWFKPYSLDWDYLFPSGWKYRDIQAAIGRVFSRIPGTDAPSTDGKRYYQQGFDVLAGGL : 405
C.therm : VLGGGTAVNAGLWWKPHPADWDDNFPHGWKSSDLADATERVFSRIPGTWHPSQDGKLYRQEGFEVISQGL : 401
H.haema : VLGGGTAVNAGLWWKPYNLDWDYNFPRGWKSRDMAAATRRVFSRIPGTDNPSMDGKRYLQQGFEILAGGL : 415
M.therm : VLGGGTAVNAGLWFKPYSLDWDYLFPDGWKYNDVQPAINRALSRIPGTDAPSTDGKRYYQEGFEVLSKGL : 403
N.crass : VLGGGTAINAGLWYKPYTKDWDYLFPSGWKGSDIAGATSRALSRIPGTTTPSQDGKRYLQQGFEVLANGL : 405
S.bisby : VLGGGTAVNAGLWWKPNPIDWDYNFPSGWKSSEMIGATNRVFSRIGGTTVPSQDGKTYYQQGFNVLSSGL : 403

                  *       440         *       460         *       480         *
C.attro : SAGGWNKVTANSSPDKKNRTFSNAPFMFSGGERGGPLATYLTSAKKRSNFNLWLNTSVKRVIREGGHVTG : 475
C.therm : ANAGWREVDANQEPSEKNRTYSHSVFMFSGGERGGPLATYLASAAQRSNFNLWVNTSVRRAIRTGPRVSG : 471
H.haema : KAAGWTEVTANDAPNKKNHTYSHSPFMFSGGERGGPMGTYLVSASRRKNFHLWTGTAVKRVVRTGGHITG : 485
M.therm : AAGGWTSVTANNAPDKKNRTFAHAPFMFAGGERNGPLGTYFQTAKKRNNFDVWLNTSVKRVIREGGHITG : 473
N.crass : KASGWKEVDSLKDSEQKNRTFSHTSYMYINGERGGPLATYLVSAKKRSNFKLWLNTAVKRVIREGGHITG : 475
S.bisby : KAAGWTSVSLNNAPAQRNRTYGAGPFMFSGGERGGPLATYLATAKKRGNFDLWTNTQVKRVIRQGGHVTG : 473

                500         *       520         *       540         *       560
C.attro : VEVEPFRTGGYQGIVNVTAVSGRVVLSAGTFGSAKILLRGGIGPADQLEVVKASKIDGPTMISNASWIPL : 545
C.therm : VELECLADGGFNGTVNLKEGGG-VIFSAGAFGSAKLLLRSGIGPEDQLEIVASS-KDGETFISKNDWIKL : 539
H.haema : LEVEPFVNGGYTGVVNVTSITGRVVLSAGAFGSAKILLRSGIGPEDQLEIVKSS-TDGPTMISDSSWITL : 554
M.therm : VEVEPFRDGGYEGIVPVTKVTGRVILSAGTFGSAKILLRSGIGPEDQLEVVAASEKDGPTMIGNSSWINL : 543
N.crass : VEVEAFRNGGYSGIIPVTNTTGRVVLSAGTFGSAKILLRSGIGPKDQLEVVKAS-ADGPTMVSNSSWIDL : 544
S.bisby : VEVENYNGDGYKGTVKVTPVSGRVVLSAGTFGSAKLLLRSGIGPKDQLAIVKNS-TDGPTMASERDWINL : 542
```

Fig. 3 Continuation

```
                  *       580         *       600         *       620         *
C.attro : PVGYNLDDHLNTDTVITHPDVAFYDFYEAWNTPIEADKNSYLSSRTGILAQAAPNIGPMMWEEIKGADGI : 615
C.therm : PVGHNLIDHLNTDLIITHPDVVFYDFYAAWDNPITEDKEAYLNSRSGILAQAAPNIGPLMWEEVTPSDGI : 609
H.haema : PVGYNLEDHTNTDTVVTHPDVVFYDFYEAG-HPNVTDKDLYLNSRAGILAQAAPNIGPMFWEEIKGRDGV : 623
M.therm : PVGYNLDDHLNTDTVISHPDVVFYDFYEAWDDPIESDKNSYLESRTGILAQAAPNIGPMFWEEIVGADGI : 613
N.crass : PVGHNLVDHTNTDTVIQHNNVTFYDFYKAWDNPNTTDMNLYLNGRSGIFAQAAPNIGPLFWEEITGADGI : 614
S.bisby : PVGYNLEDHTNTDIVISHPDVVHYDFYEAWTASIESDKTAYLGKRSGILAQAAPNIGPLFFDEVRGADNI : 612

                640         *       660         *       680         *       700
C.attro : VRQLQWTARVEG-SFDTPNGQAMTISQYLGRGATSRGRMTITPSLTTVVSDVPYLKDPNDKEAVIQGIVN : 684
C.therm : TRQFQWTCRVEGDSSKTNSTHAMTLSQYLGRGVVSRGRMGITSGLTTTVAEHPYLHNDGDLEAVIQGIQN : 679
H.haema : VRQLQWTARVEG-SAGTPNGYAMTMSQYLGRGAKSRGRMTITKALTTVVSTVPYLQDKNDVEAVIQGIKN : 692
M.therm : VRQLQWTARVEG-SLGAPNGHTMTMSQYLGRGATSRGRMTITPSLTTIVSDVPYLKDPNDKEAVIQGIIN : 682
N.crass : VRQLHWTARVEG-SFETPDGYAMTMSQYLGRGATSRGRMTLSPTLNTVVSDLPYLKDPNDKAAVVQGIVN : 683
S.bisby : VRSIQYTARVEG-NSVVPNGKAMVISQYLGRGAVSRGRMTISQGLNTIVSTAPYLSNVNDLEAVIKSLEN : 681

                  *       720         *       740         *       760         *
C.attro : LQNALKN-VAGLTWTYPNSSITPREYVDNMVVSPSNRRANHWMGTAKIGTDDGRLAGGSAVVDLNTKVYG : 753
C.therm : VVDALSQ-VPDLEWVLPPPNTTVEEYVNSLIVSPANRRANHWMGTAKMGLDDGR-SGGSAVVDLNTKVYG : 747
H.haema : LQAALSN-VKNLTWAYPPSNTTVEDFVNNMLVSYTNRRSNHWIGTNKLGTDDGRSRGGSAVVDLNTKVYG : 761
M.therm : LQNALQN-VANLTWLFPNSTITPREYVESMVVSPSNRRSNHWMGTNKLGTDDGR-KGGSAVVDLDTRVYG : 750
N.crass : LQKALAN-VKGLTWAYPSANQTAADFVDKQPVTYQSRRSNHWMGTNKMGTDDGR-SGGTAVVDTNTRVYG : 751
S.bisby : IANSLTSKVKNLKIEWPASGTSIRDHVTNMPLDPATRRANHWIGTNKIGTKNGRLTGGDSVVDLNTKVYG : 751

                780         *       800         *       820         *       840
C.attro : TDNLFVVDASIFPGTPTTNPSAYIVTAAEHASQRILGLAAPKPVGKWGQCGGRQWTGSFQCVSGTKCEVV : 823
C.therm : TDNLFVVDASIFPGMSTGNPSAMIVIVAEQAAQRILSLRY------------------------------ : 787
H.haema : TDNLFVVDAGIFPGHITTNPTSYIVIAAERASERILDLPPARAQPRFAQCGGRTWTGSFQCAAPYTCQYR : 831
M.therm : TDNLFVIDASIFPGVPTTNPTSYIVVAAEHASSRILALPDLEPVPKYGQCGGREWTGSFVCADGSTCEYQ : 820
N.crass : TDNLYVVDASIFPGVPTTNPTAYIVVAAEHAAAKILAQPANEAVPKWGWCGGPTYTGSQTCQAPYKCEKQ : 821
S.bisby : TDNLFVVDASIFPGMVTTNPSAYIVIAAEHAASKILSLPTAKAAAKYEQCGGLEYNGNFQCASGLTCTWL : 821
```

Fig. 3 Continuation

```
C.attro : NEWYSQCL : 831
C.therm : --------- :   -
H.haema : NERYSQCR : 839
M.therm : NEWYSQCL : 828
N.crass : NDWYWQCV : 829
S.bisby : NDYYWQCT : 829
```

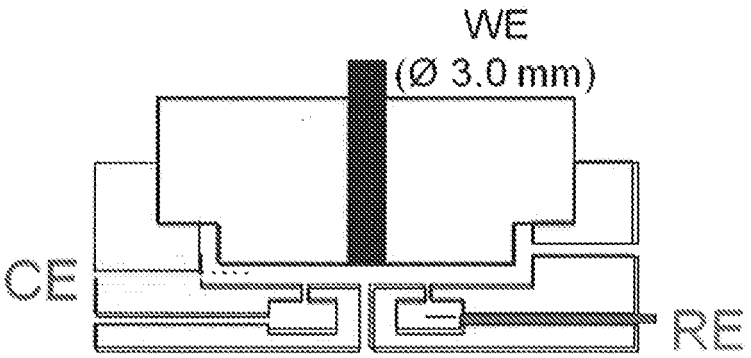
WE
(Ø 3.0 mm)
CE
RE

Fig. 4

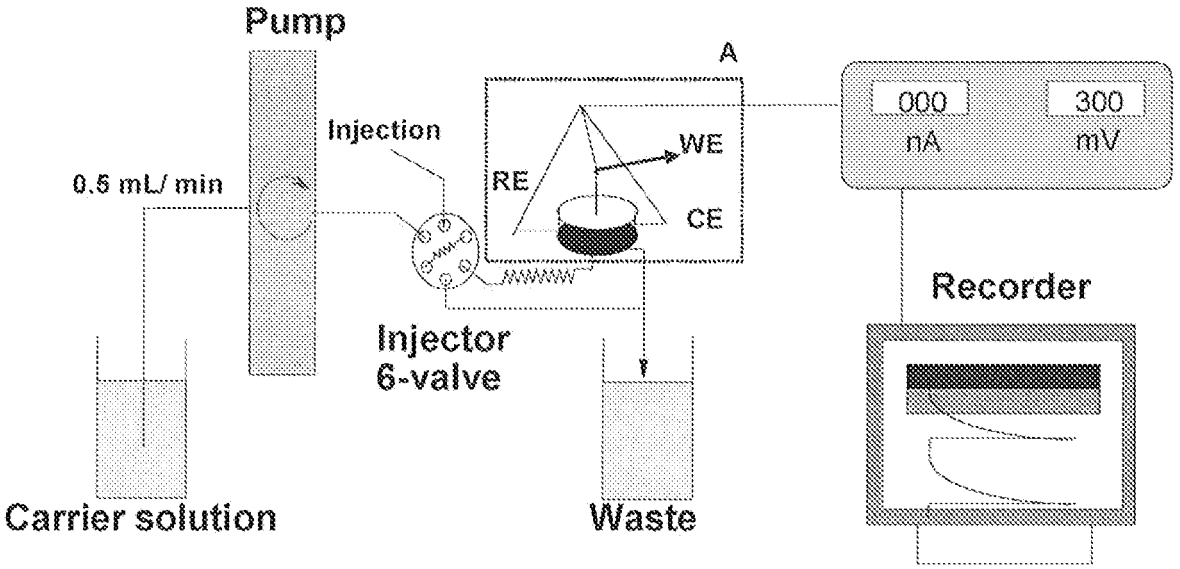
Pump
A
Injection
WE
RE
CE
000
nA
300
mV
0.5 mL/ min
Recorder
Injector
6-valve
Carrier solution
Waste

Fig. 5

Europäisches Patentamt
European Patent Office
Office européen des brevets

EUROPEAN SEARCH REPORT

Application Number
EP 09 15 3889

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
X	DATABASE EMBL [Online] 15 July 1998 (1998-07-15), "Thielavia heterothallica cellobiose dehydrogenase (cdh) mRNA, complete cds." XP002523647 retrieved from EBI accession no. EMBL:AF074951 Database accession no. AF074951 * abstract * -----	7	INV. C07K14/37
X	HARREITHER WOLFGANG ET AL: "Investigation of graphite electrodes modified with cellobiose dehydrogenase from the ascomycete Myriococcum thermophilum" ELECTROANALYSIS, vol. 19, no. 2-3, January 2007 (2007-01), pages 172-180, XP009115343 ISSN: 1040-0397 Items 2.9, 3.3-4. -----	1,2,4,7,8	
X	DATABASE Geneseq [Online] 12 June 2000 (2000-06-12), "Humicola insolens cellobiose dehydrogenase SEQ ID NO:2." XP002524037 retrieved from EBI accession no. GSP:AAY82220 Database accession no. AAY82220 * abstract * -& DATABASE Geneseq [Online] 12 June 2000 (2000-06-12), "Humicola insolens cellobiose dehydrogenase encoding cDNA SEQ ID NO:1." XP002524038 retrieved from EBI accession no. GSN:AAZ95701 Database accession no. AAZ95701 * abstract * -/--	2,7	TECHNICAL FIELDS SEARCHED (IPC) C07K

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
Munich	17 April 2009	Simm, Mariola

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons

& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04C01)

Europäisches Patentamt
European Patent Office
Office européen des brevets

EUROPEAN SEARCH REPORT

Application Number
EP 09 15 3889

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (IPC)
X	-& US 6 033 891 A (GOLIGHTLY ELIZABETH [US] ET AL) 7 March 2000 (2000-03-07) Fig. 2 and column 26. * the whole document * -----	2,7	
X	ZAMOCKY M ET AL: "Cloning, sequence analysis and heterologous expression in Pichia pastoris of a gene encoding a thermostable cellobiose dehydrogenase from Myriococcum thermophilum" PROTEIN EXPRESSION AND PURIFICATION, ACADEMIC PRESS, SAN DIEGO, CA, vol. 59, no. 2, 1 June 2008 (2008-06-01), pages 258-265, XP022637184 ISSN: 1046-5928 [retrieved on 2008-02-29] Fig. 3	1,2,4,7	
X	-& DATABASE UniProt [Online] 26 February 2008 (2008-02-26), "SubName: Full=Cellobiose dehydrogenase;" XP002523646 retrieved from EBI accession no. UNIPROT:A9XK88 Database accession no. A9XK88 * abstract * -----	4	TECHNICAL FIELDS SEARCHED (IPC)
A	ZAMOCKY M ET AL: "Cellobiose dehydrogenase - A flavocytochrome from wood-degrading, phytopathogenic and saprotropic fungi" CURRENT PROTEIN AND PEPTIDE SCIENCE 200606 NL, vol. 7, no. 3, June 2006 (2006-06), pages 255-280, XP009115339 ISSN: 1389-2037 -----		

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
Munich	17 April 2009	Simm, Mariola

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
Y : particularly relevant if combined with another document of the same category
A : technological background
O : non-written disclosure
P : intermediate document

T : theory or principle underlying the invention
E : earlier patent document, but published on, or after the filing date
D : document cited in the application
L : document cited for other reasons
.....
& : member of the same patent family, corresponding document

EPO FORM 1503 03.82 (P04C01)

ANNEX TO THE EUROPEAN SEARCH REPORT ON EUROPEAN PATENT APPLICATION NO. EP 09 15 3889

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

17-04-2009

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
US 6033891 A	07-03-2000	US 6280976 B1	28-08-2001

EPO FORM P0459

For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

Non-patent literature cited in the description

- **Stoica et al.** *Biosensors and Bioelectronics,* 2005, vol. 20, 2010-2018 **[0002]**
- **Harreither et al.** *Electroanalysis,* 2007, vol. 19, 172-180 **[0002] [0004] [0098] [0099]**
- **Henriksson et al.** *Biochimica Biophysica Acta,* 1998, vol. 1383, 48-54 **[0002]**
- **Lindgren et al.** *Analyst,* 1999, vol. 124, 527-532 **[0003]**
- **Stoica et al.** *Analytical Chemistry,* 2004, vol. 76, 4690-4696 **[0003]**
- **Schou et al.** *Biochemical Journal,* 1998, vol. 330, 565-571 **[0004]**
- **Lindgren et al.** *Journal of Electroanalytical Chemistry,* 2001, vol. 496, 76-81 **[0004]**
- **Henriksson et al.** *Biochimica and Biophysica Acta,* 1998, vol. 1383, 48-54 **[0011]**
- **Schou et al.** Humicola insolens CDH: no glucose conversion detected. *Biochemical Journal,* 1998, vol. 330, 565-571 **[0011]**
- **Ludwig et al.** *Applied Microbiology and Biotechnology,* 2004, vol. 64, 213-222 **[0011]**
- **Karapetyan et al.** *Journal of Biotechnology,* 2005, vol. 121, 34-48 **[0066]**
- **Canevascini et al.** *European Journal of Biochemistry,* 1991, vol. 198, 43-52 **[0067]**
- **Sachslehner et al.** *Applied Biochemistry and Biotechnology,* 1997, vol. 6365, 189-201 **[0073]**
- **Liu et al.** *Journal of Clinical Microbiology,* 2000, vol. 38, 471 **[0075]**
- **Appelqvist et al.** *Anal. Chim. Acta,* 1985, vol. 169, 237-47 **[0081]**
- **Ruzicka ; Hansen.** Flow Injection Analysis. Wiley, 1988 **[0087]**
- **Zámocky et al.** *Current Protein and Peptide Science,* 2006, vol. 7, 255-280 **[0096]**